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Combining Ability of Protein and Other Selected Characters With the F1 and F2 Plant Generation of Two-Way Crosses of Ten Soybean Lines.

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COMBINING ABILITY OF PROTEIN AND OTHER SELECTED CHARACTERS WITH THE F_1 AND F_2 PLANT GENERATION OF TWO-WAY CROSSES OF TEN SOYBEAN LINES

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ABSTRACT

A study was conducted in Baton Rouge in 1973 with 10 lines of soybeans (Glycine max (L.) Merrill) differing widely in protein content to determine F_1 hybrid performance and the heritability and relative combining ability of protein and other selected characters in the F_2 generation. Forty-five crosses were made between these parental lines, in all combinations, using the high protein parent where possible, as the female.

Significant differences were found among some of the parents grown with the F_1 and F_2 populations for protein content, maturity date, plant height, and flowering date. Significant differences were also found among the F_1 and F_2 progeny, for all characters mentioned above.

Protein content in both the F_1 and F_2 progeny tended to be more like the high protein parent. Heterosis for protein in 13 F_1 hybrids averaged about 1% above the high parent. Highest specific combining ability for protein was indicated by the F_1 progeny of D67-6117 x Tracy and D68-4641 x Hutton. They exceeded the high protein parent by 1.05 and .79% protein, respectively. Some F_2 progeny were above and some below two standard deviations of their respective F_2 protein mean. Maternal and cytoplasmic effects may have caused some of the F_1 and F_2 progeny to be skewed toward the high protein parent since the high protein parent was used as the female in most cases.

Although maturity date in the F_1 progeny tended to be more like the late maturing parent, there were a greater number of F_2 progeny that were more like the earlier maturing parent. Heterosis for maturity date was indicated by F_1 progeny exceeding the later parent by at least two days.

Plant height in the F_1 progeny tended to be more like the taller parent but, the F_2 progeny tended to be more like the shorter parent. Heterosis for plant height in the F_1 progeny averaged 4.2 cm above the taller parent. Best specific combining ability for plant height in the F_1 progeny was indicated by Tracy x Pickett 71 and D67-6117 x Tracy. They exceeded the taller parent by 7.86 and 7.79 cm, respectively.

Flowering date in the F_2 progeny tended to be more like the earlier flowering parent.

Transgressive segregation occurred in the F_2 progeny of some cross combinations for protein (mostly higher), maturity date (generally earlier), plant height (usually shorter), and flowering date (mostly earlier).

The data that additive and other gene action was involved in controlling the above mentioned characters.

Heritabilities as an average of all lines for protein, maturity date, plant height, flowering date, and height of lower pod were .70, .50, .63, .76, and .46, respectively.

The expected advance indicated the progeny of three crosses, all high protein x high protein, had F_3 predicted means of over 52% protein.

The general low or lack of association between the correlation coefficients of the characters flowering date, maturity date, and plant

height with yield or protein indicated that little or no progress could be made in improving the yield or protein by selecting for the above mentioned characters in the F_2 generation.

Three methods for determining protein in soybeans were compared. Correlation coefficients of .96**, .94**, and .93** were all highly significant and indicated a strong association between the three methods.

INTRODUCTION

The soybean (Glycine max. (L.) Merrill), is believed to have originated in the Eastern and Northern parts of China. Its importance to the Chinese can be seen by the fact that it was classified as one of the five sacred grains of China and essential to the existence of the Chinese civilization. The Chinese used different products made from the seeds of soybeans. The seeds have long been used in the preparation of a large variety of fresh, dried, and fermented food products. From China, the cultivated soybean spread to other countries, until today it is grown in almost every country whose climate will allow its cultivation (69).

Soybeans were introduced into the United States as early as 1804 (61, 69). Its early uses in the United States were as a forage crop and to some extent as a green manure (69). By 1890 most of the experiment stations in the United States had conducted experiments with the soybean, but it was not until the 1930's that it generated much attention (61). Osborne's work on seed proteins, which began in 1891, helped make researchers aware of the importance of protein in the seeds of soybeans. Mooers (60), in 1908, recognized the value of soybeans to farmers for its potential in the production of protein and oil. In 1924, Hacklemann (34) stated that the most profitable outlet for the production of soybeans would be as a seed crop. He also classified soybeans as the best annual nitrogenous seed producing plant.

As research with soybean protein continued, many new uses for it were found. Presently, rather than being only an additive to animal

feed, soy proteins are added to many types of human foods. These new soy protein products can be obtained from most supermarkets in many different forms. Soy protein is so acceptable today that many consumers are unaware that it is added to many of the foods they consume.

The major consumption of soybean protein in the United States is by livestock with poultry and hogs using about 60% of the soybean meal.

Soybean cultivars currently grown in the United States range from about 39% to 43% seed protein on a dry weight basis. However, the Souix cultivar has a seed protein content of about 52% on a dry weight basis. Soybean breeding lines with moderately high yield have been developed with protein contents of 45 to 46%. As world population increases, demand for protein will increase. Protein production per acre can be increased in several ways, one of which is increasing the protein content of the seed while maintaining yield at the current level.

The purpose of this research was to study: 1) the performance of two-way F_1 hybrids from crosses differing widely in protein content, 2) the heritability of protein and other selected characters in the F_2 generation derived from crosses of lines of high, medium, and low protein, and 3) the relative combining ability of these parent lines for protein and selected characters.

REVIEW OF LITERATURE

T. B. Osborne (65) studied seed proteins from 1891 until the late 1920's. His classification, which is based on the solubility of seed proteins, is still being used today. Seed proteins are classified in the following manner: 1) globulins, those that are insoluble in water but soluble in saline solutions; 2) albumins, those that are soluble in water; 3) prolamines, those that are soluble in relatively strong alcohols; and 4) glutelins, those that are soluble in dilute alkaline solutions but not in water, saline, or alcohol solutions. Globulins constitute the bulk of the storage proteins in soybean seeds (24, 63, 65, 77). Ultracentrifugal and other methods of fractionation revealed that at least 4 components, 2, 7, 11, and 15S, are present (62, 97). Taira and Taira (81) classified protein components in the following way: A (2 S component and soybean trypain inhibitors), B, C, and D (11 S components), and E (7 S component).

Caldwell and Hanson (14) studied the possible effects of different soybean stem and root genotypes on the accumulation of protein and oil content of the seed. Reciprocal grafts were made between different genotypes which varied in protein and oil percentages. They concluded that the control sites for protein and oil synthesis were located in the above ground portion of the plant, since root genotypes did not have any effect on the protein or oil content of the seed.

Bernard and Weiss in 1973 (5) reported that the inheritance of soybean protein appeared to be polygenically controlled. However, there have also been reports of monogenically controlled differences between

seed proteins (21, 42, 47, 48, 49, 76). Larsen (47) analyzed 61 soybean varieties by disc electrophoresis for seed proteins. He found that there were two components revealed by the stained proteins that separated the varieties into two major groups. These were classified as component "A," which was present in 13 varieties, and component "B" which was present in 48 varieties. There were no instances observed where components A and B were simultaneously present in a single variety. Larsen and Caldwell (48, 49) reported similar results. Their data indicated a pair of codominant genes at a single locus controlled the protein components. Heterozygous plants exhibited both "A" and "B" components of protein while homozygous plants either had the A type of protein or the B type of protein. Other studies have indicated a single codominant gene controlling a particular protein (21, 42, 76).

Breeding for Protein

Brim (9) stated that if correlations are high between two components, attempts to obtain a response in one component by selecting for an associated trait may be worthwhile. He indicated that this is especially true when a character which has a high economic value has low heritability when compared to the associated trait.

Caldwell et al. (15) found that maximum gains for total production of protein and oil were obtained from indices constructed to increase yield; yield and protein; yield and oil; and yield, protein, and oil. Selection for protein and oil alone increased their content in the seed, but drastically decreased their total production per acre.

Smith and Weber (78) suggested that soybean lines or populations could be selected for high protein or oil based on the specific gravity of the seed. They found that high seed density was associated with high protein, low oil, and late maturity.

Thorne and Fehr (82) reported that selection for protein and oil was successful for increasing the protein content of a population while maintaining the same oil level as that of the unselected population. This study involved 2- and 3-way crosses between adapted varieties and high protein exotic lines. The high protein content of exotic lines was readily transmitted to their offspring and selection of high-yielding, high-protein lines from these crosses was possible. The 3-way populations were better sources of higher-yielding, higher-protein strains than the 2-way populations.

Hartwig and Hinson (39) evaluated a selection technique based on the oil percentage of two backcross populations in selecting for yield, and protein and oil content. They found lines distinctly different in protein content by selecting strictly on the basis of oil percentage. The high protein lines averaged lower in yield than did high oil lines obtained from these backcrosses. However, the authors were convinced that the genes for high protein did not influence the yield.

Shannon et al. (72) evaluated 78 lines derived from six soybean populations to determine which population had the best potential for improving yield, protein, and yield and protein in combination. They used the following cross combinations in the test: 1 high protein x high protein; 4 high protein x high yield; and 1 high yield x high yield. Cross combinations between high protein x high protein parents produced

more lines high in percent protein and in protein per hectare. These combinations also produced more lines that combined high protein with high yield, showed the greatest expected advance for yield and protein per hectare, and was the only population in which the expected advance surpassed the parental means for protein per hectare and percent protein. Only one population from a cross combination involving a high protein x high yield parent exceeded the above population for predicted progress in percent protein.

The association between pod dehiscence and other agronomic characters including protein content were studied by Caviness (17). No serious limitations to breeding for these characters were indicated. This was especially true in crosses where both parents were classified as Glycine max. (L.) Merrill.

Hadley and Hymowitz (35) observed that although there were significant differences between puberlent and pubescent segregates for protein, oil, and sugar, that this was irrespective of family indicating genetic background does not significantly affect the relationship between chemical composition and pubescent types. Pubescent types did not affect either heritability estimates or correlation coefficients involving chemical composition of the seed.

The Effect of Certain Factors on Protein

Collins and Cartter (22) found seeds on the upper half of the plant were 1% higher in protein than those in the lower half and seed near the tips of long terminal racemes had more protein than average. Beans in the tip of the pods had lower protein and higher oil when compared to other beans in the pods.

A study by Hanson et al. (37) on the effects of competition on protein and oil percent indicated that the protein percent was not markedly affected by competitive effects between plants.

Donovan et al. (25), in a study of the effects of planting patterns on protein percent, oil percent, and yield, found that protein content of the seed was only slightly affected by spacing although it was highest at closest spacing. The best row spacing for a combination of both protein and oil was 7-inch rows with 4-inch spacing between plants.

Climatic factors did not greatly influence the protein content of the varieties tested by Cartter and Hopper (16).

Weiss et al. (93) and Torrie and Briggs (83) found that date of planting did not affect protein content of soybean seed. In a later study by Weiss et al. (94) similar results were reported. However, they found that for two of the five varieties studied, there was an association between lateness of maturity and low protein content.

The highest oil content was obtained by Osler and Cartter (66) from the earliest planting date and it decreased progressively thereafter as the planting date was delayed. Also protein varied inversely with oil content. The inverse relationship between protein and oil content of soybean seed has been reported by many other researchers (3, 6, 7, 8, 22, 27, 36, 45, 66, 67, 80, 93, 94).

Neither planting date nor location had much influence on protein or oil content of soybean seed in a test in Tennessee (33). However, the earliest and latest planting dates produced seed with the most protein and the least oil as an average of all locations and years.

Agrawal and Vyas (1) found that when the mean temperature increased from the 50% flowering stage to harvest, the protein content of the seed decreased and the oil content increased. They also found a highly negative correlation between percent protein and mean temperature, and a highly positive correlation between percent oil and mean temperature.

Taira and Taira (81) studied the influence of three different locations on the protein components (A, B, C, D, (11S), and E (7 S), of the soybean seed. Their data showed that location had very little effect on the percentages of each of these components.

Lipman and Blair (52, 53, 54) obtained higher yields and increased the protein content of soybean seed by inoculating the seed prior to planting. Also, the addition of lime to the soil increased yield and protein content of the seed. Similar results were reported by Fellers (27). Increased yields and in some instances higher protein content were obtained from differing amounts of applied nitrate, phosphorus, potassium, and sulfur.

Zahnley (98) reported that inoculation of soybean seeds increased the protein content of the seed by 4.2% and in the hay by 1.19%. The yield of the seed was also increased by 24% and the hay yield was increased by 42%.

Hackleman (34) stated that the addition of limestone to the soil must be recognized as an essential part of the successful production of soybeans.

Stark (80) observed that the addition of limestone and organic matter to the soil increased the protein content and decreased oil content of the seed. Although the oil percentage of the seed was less, the total production in oil per acre was increased.

Jones and Lutz (44) found that deep placement of lime in fine textured subsoils did not increase protein content or yield of the seed, but did significantly increase the oil content.

Chesney (20) studied the effects of nitrogen, phosphorous, and potash on soybeans grown in wet tropic soils. The results clearly indicated that N, P, and K did not influence the protein or oil content of the seeds when grown in those particular tropic soils.

Kang (45) observed that inoculation alone was inadequate in supplying the nitrogen needs of the soybean crop. The requirements observed for maximum yield were 30 kg/ha when the seeds were inoculated and 60 kg/ha without inoculation. Higher nitrogen applications combined with inoculation increased the protein content of the seed, yield, number of pods per stalk, and bean weight but decreased oil content.

Lutz and Jones (55) reported that protein content was unaffected by irrigation. However, irrigation did increase the oil content and the yield of the seed was increased by 22%. The addition of phosphorous and potassium did not affect yield the first two years the experiment was conducted, but where they were not applied to the plow sole the third year, the yields were lower.

Ham et al. (36) demonstrated that the addition of nitrogen fertilizer increased seed protein percentage and kg protein/ha, seed yield, and seed weight. Seed oil content was decreased as the amount of added nitrogen increased. An increase in both seed protein and yield indicated nitrogen fixation in nodulating lines failed to supply a sufficient amount of nitrogen needed for maximum seed and protein yields.

Chatt et al. (19) reported that Mo is a constituent of the nitrogen fixation enzyme, nitrogenase; and functions in the fixation of nitrogen by weakening the dinitrogen bond.

Leaf nitrogen and seed protein, weight, and yield were increased by the application of Mo or lime to moderately acid soil while the oil content was reduced (67). Also, a significant positive correlation occurred between seed yield and leaf nitrogen, leaf nitrogen and seed protein, seed yield and seed protein, seed yield and seed weight; and where Mo was not applied, seed yield and soil pH.

Boswell and Anderson (6) stated that the application of Mo to soybeans increased the protein content of the seed and also the nitrogen and Mo content of the leaves. A highly significant negative correlation between protein and oil content of the seed was observed when various Mo treatments were applied.

Boswell and Worthington (7) found that there was a tendency for the percent protein to increase slightly as the rate of boron increased up to .56 kg/ha. However, this increase was not a significant increase. They concluded that different soil sites and years affected total protein and oil percentages of the seeds more than the boron.

Touchton and Boswell (84) observed that the application of B to soybeans did not affect the protein and oil percentage, nodule formation, or seed size. However, they did observe an increase of B in mature seed as the rate of B applied increased.

Heritability and Correlation Among Characters

Weber and Moorthy (92) studied the heritability of flowering time, maturity date, period from flowering to maturity, plant height, and seed weight. The parents and their F_1 and F_2 were used in a study and data was taken on an individual plant basis. The parents were chosen on the basis of their differences in oil content. They reported that environmental factors accounted for the major portion of total variability in seed yield, and that the other characters studied were less affected by soil and environmental variations. The highest heritability was found for flowering date (76%) and the lowest for seed weight (54%). A positive association occurred between yield and plant height, yield and maturity date, and flowering time and maturity date.

Johnson et al. (43) conducted genetic and environmental variability studies using the F_4 and F_5 soybean lines at several locations for one year and two year periods. They reported the following: 1) estimates of genetic variance obtained in different environments had less consistency for yield than for other important characters; 2) estimates of genotype x environment interactions were higher for yield than for other important characters; and 3) heritability of yield was lower than for other important characters. Expected genetic advance was found to be higher for yield than for percent protein and oil.

Anand and Torrie (3) calculated heritability estimates for the progeny of three crosses grown in the F_3 and F_4 generations. They obtained low heritability estimates for seed yield, pods per plant, and seeds per pod. Heritability estimates for seed weight, lodging, height, days to flowering, fruiting, and maturity were generally high.

Hanson et al. (38) divided genetic variability into additive x additive and total genetic variance. They found considerable additive x additive epistatic variability for seed yield and maturity which accounted for more than 50% of the total genetic variance. They detected only a moderate amount of epistatic variability (20%) for plant height and lodging. Those characters exhibiting additive genetic variance were: seed weight, percent protein, seed quality, percent oil, and downy mildew.

Caviness and Prongsirivthana (18) reported evidence that a high degree of phenotypic dominance was responsible for node number and plant height in a cross between Lee x R61-900. A single major gene pair appeared to control the number of nodes on the main stem. Higher heritability estimates were obtained for plant height than for average internode length. They isolated true breeding plants which were less than 90 cm in height that contained more than 20 nodes on the main stem.

Croissant and Torrie (23) found that the major component of genotypic variance for all economically important characters of soybeans was additive genetic variance. Dominance components were found for plant height, seed weight, and lodging, but were relatively small when compared to total genetic variance. Estimates of linkage components were obtained and appeared to be important for days to flowering, seed weight, plant height, and lodging, but not for seed yield. Gates et al. (31) reported similar findings. However, they also found linkage to be significant for yield.

Brim and Cockerham (10) evaluated the parent and F_1's from two crosses in replicated yield trials in two locations for two years.

The F_1's were found to be significantly greater than the high parent for height and yield in one cross, and only for yield in the other cross. Inbreeding depression for advanced generations (F_2-F_5) was neither great nor very consistent. Additive variance was the major component of genetic variance.

Weber et al. (91) measured heterosis by comparing the F_1's from 85 crosses with their respective parents in four years. The seed yield of the F_1's averaged 13.4% more than their respective high parents of the crosses. Nearly 77% of the F_1's exceeded the high parent for yield. The F_1 hybrids approximated the midparent average in maturity and did not vary significantly from the midparent mean in protein or oil content. The F_1's were generally shorter than the taller parent. Gene action other than additive was indicated for yield.

Brim (9) cites examples of findings by others that in most instances homozygous lines are obtained that outperform the F_1 hybrid in all economically important characters.

Gopani and Kabaria (32) conducted a heritability study on yield in which they also reported correlations between yield and other characters. They found that the highly heritable characters in their study were: number of seeds, number of branches, seed weight, and oil content. Yield was found to be significantly and positively correlated with number of seed, number of pods, and number of branches per stalk. They also found that regression of yield on number of seed per plant was highly significant.

Martin and Wilcox (58) obtained moderately high heritability of height of lower pods from three crosses. The higher the height of the lowest pod, the later the plant flowered and matured. The lack of

association between pod height and seed yield indicated that selections could be made for increased height of lower pod without affecting yield.

Weatherspoon and Wentz (90) reported a significant positive correlation between yield and plant height, number of pods per plant, number of nodes per plant, and number of pods per node. The most important characters in estimating yield were number of nodes per plant and plant height.

Anand and Torrie (3) found that high yield was positively correlated both phenotypically and genotypically to increased plant height, late maturity, and susceptibility to lodging. They also found a phenotypic association for yield with number of seed per pod and number of pods per plant. Similar results were reported by Kwon and Torrie (46).

Burnside and Colville (13) found a highly significant positive correlation between yield and plant height at maturity, number of pods and seeds per plant, lodging, seed-bearing nodes, and weight of 100 seeds. Characters showing a highly negative correlation with yield were bushel weight, oil percent of the seed, and height of lowest pod. Thorne and Fehr (82) reported a negative correlation between yield and protein percent in all of their population studies.

Saxena and Pandey (71) obtained a high positive correlation between grain yield, and number of pods per plant, weight of 100 seeds, and days from planting to maturity ($r = +0.95$). The first two components were more highly correlated with yield than was the last component.

Effect of Time of Planting on Components

Weiss et al. (93) determined the effect five planting dates had on different soybean characters. Maturity date was retarded more in early varieties by planting at later dates than it was in later maturing varieties. Maximum plant height was attained at the second date of planting and decreased with successively later plantings. Yields decreased more in earlier maturing varieties with progressively delayed planting dates after May 1. In a similar study of five planting dates, the following characters were significantly correlated: lateness of maturity with low oil content, days from flowering to maturity with low oil content, days from flowering to maturity with high oil content, high mean temperature with high oil content, and high protein content with low oil content. Similar observations were made by other research workers (50, 79).

Osler and Cartter (66) found that when planting dates were progressively delayed, maximum plant height and oil content were progressively decreased and maturity date was delayed more for early maturing varieties than for later maturing ones.

Torrie and Briggs (83) reported that protein content was unaffected by planting date. Also, all varieties responded similarly in the retardation of their maturity dates with each delay in planting date. However, plant height reacted the same way it had in the previous experiments.

Spacing Effects on Yield and Other Characters

Wiggins (95) obtained a yield decrease with any and all increases in distance between rows from 8 to 32 inches. The distance between plants within rows from 1/2 to 6 inches had little effect on yield and maturity. Probst (68) observed that highest yields were obtained when plants were spaced from 2-3 inches apart within rows.

Frans (29) concluded that 10- and 7-inch row spacings produced the highest yields in two out of the three years in Arkansas tests.

Lehman and Lambert (51) used two-row spacings (20 and 40 inches) and four-plant spacings within rows (4, 8, 16, and 24 plants per linear foot). Yields tended to be greater at the narrow row spacing. Their yield data for within-row spacing was too variable to be conclusive. They found that as spacing increased, the seeds per pod, seeds per plant, pods per plant, and number of branches per plant also increased.

Donovan et al. (25) tested the performance of a soybean variety, Mandarin, using 15 planting patterns which resulted in five row spacings (7, 14, 21, 28, 35 inches) and three-plant spacings (1, 2, 3 inches) within the rows. This test was conducted over a four-year period. They reported that the narrowest rows with the widest plant spacing gave the highest yields.

Mauro et al. (59) studied the effects of row spacing on several soybean characters. They used four-row spacings (25, 50, 75, 100 cm) and four planting rates (8, 16, 24, 32 plants per meter) in this experiment. They concluded that in both cultivars, seed yields increased as row spacing decreased, with the highest yields obtained for the 25 cm row spacing. However, they did not detect any yield

differences for different plant spacings within rows. They stated that plant height, height of lowest pod, and lodging increased as the distance between rows decreased and planting rates increased.

Wilcox (96) also observed an increase in plant height, height of lowest pod, and lodging with an increase in plant population. He said that some soybean strains did not react alike in yielding ability at different population densities although some were consistent in yield at all population densities. Population density did not have any apparent effect on maturity date.

Basnet et al. (4) reported that the height of lowest pod increased as row width and within-row spacing decreased. They found that as plant density increased in both row width and plant spacing, the plants were taller, lodged more, and produced fewer nodes. Also, these plants produced fewer branches, pods on branches, pods on main stem, and total seeds on an individual plant basis. Highest yields were obtained one year from the lowest plant density in narrow rows, and the next year at the highest plant density in wider rows.

Maternal and Cytoplasmic Influence on Oil and Protein

Brim et al. (11) studied the maternal effect on fatty acid composition and oil content of soybeans in three groups of reciprocal crosses. The genotype of the maternal parent was primarily responsible for oil content and fatty acids of the oil. The pollen parent had little influence on the linoleic and oleic acid content of the seed oil. However, in certain crosses, the genotype of the male parent had an influence on the linoleic acid content.

Singh and Hadley (73) found significant differences in oil content between P_1 and $P_1 \times P_2$ on P_1 plants and between P_2 and $P_2 \times P_1$ seed on P_2 plants in nine out of the twelve comparisons made. They did not detect any cytoplasmic effects. They concluded that oil synthesis in soybean seed is determined largely by the genotype of the plant producing the seed.

Garwood et al. (30) conducted a similar study with corn and found differences in oil content of F_2 kernels born on F_1 plants from reciprocal crosses. They concluded that these differences were caused by cytoplasmic effects.

Singh and Hadley (74) determined the protein content of individual seeds from F_1, F_2, backcross, and parental populations by micro-Kjeldahl. The parental populations involved included both high and low protein varieties. They found that the mean protein percent of F_1 seeds did not differ from that of the selfed seeds produced on the same plant indicating strong maternal effects. A significant increase of three to four percent associated with cytoplasms from the high protein lines was observed for the overall means of two pairs of reciprocal crosses obtained from F_2 and backcross seeds. The authors attributed this to be the result of maternal cytoplasmic effects. Variances of selfed seeds on plants of both high and low protein parental lines were as large as variances of selfed seeds on F_1 plants from crosses between these lines. The results suggest that the genotype of a soybean seed has little influence on the percent protein of the seed.

Methods of Protein and Oil Analysis

Fehr et al. (26) concluded that the Kjeldahl method was superior to seed density or specific gravity methods for direct measurement of protein. Nuclear magnetic resonance was found to be superior to solvent extraction as a rapid and accurate method of oil analysis.

Rinne et al. (70) determined the protein and oil content of 45 samples of soybean meal with an infrared light reflectance instrument. These analyses were then compared to duplicate analyses determined by Kjeldahl and Soxhlet petroleum ether. They obtained a highly significant correlation coefficient between infrared and Kjeldahl protein of $r = 0.971$. The correlation coefficient between infrared oil analysis and Soxhlet petroleum ether extraction was also highly significant ($r = 0.977$).

Hymowitz et al. (41) used a grain analyzer consisting of a near-infrared light instrument coupled to an analog computer to give simultaneous estimates of protein and oil content in soybeans, corn, and oat seed meals. These estimates for protein and oil were then compared to protein and oil determinations by Kjeldahl and nuclear magnetic resonance, respectively. Multiple correlations between Kjeldahl protein and the infrared analyzer were .996 for soybeans, .994 for corn, and .982 for oats. Correlations between grain analyzer oil determination and nuclear magnetic resonance for soybeans, corn, and oats were .992, .993, and .990, respectively.

Fraenkel-Conrat and Cooper (28) were the first to report finding a quantitative reaction between protein and orange-G dye at a pH of 2.2. They theorized that the dye formed an insoluble complex with free

amino groups, lysine, the imidazole group of histidine and the guanidyl group of arginine.

Udy (85, 86, 87, 89) refined the dye binding method and adapted it to measure protein in several types of agricultural products. He also organized and developed equipment to facilitate processing of these agricultural products and their protein analysis (88).

Bunyan (12) investigated the possible association between the dye-binding and standard Kjeldahl methods for determining protein. Although he found a correlation between the two methods, he did not recommend the dye-binding method for analysis of protein when accuracy was desired. He stated that estimates of protein content from the dye-binding method were inaccurate because there was variation in meals of the same type.

Olson and Heighes (64) studied the feasibility of using the dye-binding method for determining the protein content in barley. They obtained a correlation coefficient of 0.96 between the Kjeldahl and dye-binding methods. Similar results were reported by others (56).

Hymowitz et al. (40) compared the Kjeldahl to the dye-binding method for determining protein in soybeans. They used 95 soybean meal samples with protein content ranging from 27-51% determined by Kjeldahl. They reported a correlation coefficient of .985. They concluded that the dye-binding method could be used for estimating protein in soybean or for estimating Kjeldahl values.

Singh and Hymowitz (75) investigated the possibility of using the modified dye-binding method for screening soybean populations for protein content. Seed samples from 650 plants in different generations

from two sets of reciprocal crosses were used in determining protein content by Kjeldahl and modified dye-binding methods. They found the correlation coefficient between these two methods to be 0.74. They calculated the per sample cost for each method and found the modified dye-binding method to cost approximately half the cost of the Kjeldahl method.

MATERIALS AND METHODS

Ten advanced soybean lines and commercial varieties were crossed in all possible combinations, except reciprocals, during the summer of 1972. These lines and commercial varieties will henceforth be referred to as parental lines. It was assumed that these parental lines were homozygous for all characters studied. The lines, which are listed in Table 1, range in protein content from approximately 40.0 to 46.0 percent. The actual protein content will vary by location, year, laboratory, and method of analysis. The total number of cross combinations were 45. The high protein line was used as the female parent in all combinations except 4 x 1, 4 x 2, 4 x 3, 8 x 7, and 9 x 7. Singh and Hadley (74) reported strong maternal effects in soybeans. Therefore, the high protein line was chosen as the female. The qualitative characters of flower color and pubescent color were used where possible as genetic markers to determine whether a cross had actually been made by checking these characters in the F_1 generation.

Three seeds from each cross combination were planted in the greenhouse in the fall of 1972 to produce F_2 seed. These were harvested in the spring of 1973.

Seeds that would produce the F_1 and F_2 plant generations (referred to as F_1 and F_2) were planted in separate, but adjacent tests. The F_1's and parents were planted by hand on May 29 and 30, 1973, in a randomized complete block design with three replications. Rows were seven feet long and 40 inches wide. Seeds were spaced every four inches within the row. An alley three feet wide separated each plot. A plot

Table 1. Lines and cultivars used as parents and their respective flower color, pubescent color, maturity group, protein content and parentage.

Line No.	Line[1/]	F.C.[2/]	P.C.[3/]	M.G.[4/]	A.P.C.[5/]	Parentage
1	D67-6117	P	G	VII	46.00	Semmes x D60-8107
2	D69-0263	W	B	VII	46.00	Bragg (2) x D60-7965
3	F67-3673	W	B	VII	45.50	Bragg x D60-8107
4	D68-4641	W	G	V	45.00	D62-6289 x D60-9647
5	F66-698	P	G	VII	44.50	(F55-224 x D55-4073) x (F58-5788 x D56-4065)
6	Tracy	W	B	VI	43.50	D61-618 x D60-9647
7	Hutton	P	B	VIII	42.50	F55-822 x (Roanoke x CNS-4)
8	Bragg	W	B	VII	41.50	Jackson x D69-2491
9	Pickett 71	P	G	VI	40.50	Pickett x Phytophthora resistant Lee type
10	Ransom	P	B	VII	40.00	(N55-5931 x N55-3818) x D56-1185

1/"D" = lines selected at Stoneville, Miss., "F" = lines selected at Gainesville, Fla.
2/Flower color; P = purple, W = white.
3/Pubescence color; B = brown, G = grey.
4/Maturity group.
5/Approximate protein content in percent.

consisted of three rows, the P_1, F_1, and P_2, except that a P_1 was sometimes P_1 or P_2 of another F_1 combination. Parents were planted on odd numbered rows and the F_1's on even numbered rows. The F_1 seed were planted near the center of the even numbered row. Seed of the parents were planted on each end to fill out the row and provide competition. One border row was planted on each side of the test with one serving to separate the F_1 and F_2 test.

The F_2 seed from each cross combination were divided into three parts and each part considered a replication. This test was planted on June 2 and 3, 1973. The plots consisted of two rows 40 inches wide and eight feet long. Seeds were spaced four inches apart. An alley three feet wide separated the plots. The first and last plants on each row of a plot were parent plants. These plants were border and no data were taken on them. The first six plants on the first row of each plot were parent plants. Data were obtained on five of these plants. For the combinations that had fewer than 41 seeds per replication, the seeds were planted from the center of the plots with parent seeds used to complete the row.

The areas of each row planted to F_1 and F_2 plants were staked. All F_1 and F_2 plants were numbered and tagged in the field. Corresponding numbers remained on each F_1 and F_2 plant throughout this test. Wherever possible only 5 competitive parents from each plot were randomly chosen as representatives of the parents, and data were taken on these throughout the entire test. A competitive plant was classified as one flanked on either side by another plant not more than four inches away. Data were taken on all F_1's and F_2's throughout the experiment whether competitive or not.

The flowering dates (date the plant flowered after July 1) and maturity dates (date after September 1 when all pods turned brown and 90% of the leaves were dead) were recorded on all F_1, F_2, and competitively numbered parents throughout the summer and fall of 1973. The entire mature plant was removed from the soil, tagged, and stored.

This test study was grown on Olivier silt loam at the L.S.U. Perkins Road Agronomy farm, at Baton Rouge. Throughout the growing season recommended cultural practices including fertilization, weed control, and insecticide applications were followed.

During the summer of 1974, plant heights (measured in centimeters from the base of the plant at ground level to the terminal of the main stem), and height of lower pod (measured in cm from the base of the plant at ground level to the first pod on the main stem) were recorded prior to threshing each plant individually. The seeds from each plant were cleaned, placed in labelled coin envelopes, and the yield recorded (weight of seed in grams). All seeds were stored in the same location until February, 1975, when protein analysis began.

Protein Analysis

The Udy Dye Method was used for protein analysis in this test. The process consists of a known excess of the reagent dye solution being reacted with a sample forming an insoluble protein-dye complex. The remaining unreacted dye concentration was measured by colorimetric means using a Udy color analyzer. The indicated readings were then subjected to a conversion table to obtain the protein percentage of each sample. The conversion table was obtained from the Udy Analyzer Company, Boulder, Colo. A reference dye of precisely known concentration

was used to preset or calibrate the color analyzer to a reference reading prior to beginning analysis.

The following outline was the steps used in the analysis procedure:

Each sample for analysis consisted of 20 seeds randomly selected from seed of each F_1 and F_2 plant. Twenty seeds were also randomly selected from each bulk parent sample. Twenty seeds from each representative parent plant within each replication were selected and placed into one of the bulk samples. An equal number of parent plants was included in each bulk sample within each replication. There were a total of 18 bulk parent samples from the entire test for each of the parent lines (3 bulk samples for each replication). The selection of a 20 seed sample was made for several reasons: 1) In some cases, the number of progeny seed available was small, 2) samples larger than this tended to collect within the grinding mill making it very difficult to clean and causing it to overheat, 3) twenty seed samples were found to have a coefficient of variation of 1.51 percent for protein. Thus, with the short supply of seeds and the low coefficient of variation, it was determined that 20 seeds would be used for all samples.

Prior to the initiation of any protein analyses on the seed samples of this study, a bulk check sample was prepared. The seed from one variety (Hutton) were ground with a Udy cyclone mill within which a screen with .4 mm openings was installed. The entire ground bulk sample weighing approximately .5 kilograms was placed in one container, and thoroughly mixed. Each standard check sample removed from this bulked sample was treated exactly like the batch of samples it

accompanied from the drying process through the protein determination process.

Each sample was ground with a Udy Cyclone Mill. A screen with .4 mm openings was installed in the mill so that each sample was passed through it prior to being deposited in the sample jar. Milled samples were dried in a Thelco circulating dry-air oven for approximately 12 hours at 70°C. It was found that a 20 seed sample size required approximately 9 hours of drying at 70°C before the sample stopped losing weight. The samples were dried to approximately 3.98% moisture content at this temperature. The samples were removed from the dryer individually and thoroughly mixed prior to weighing. One-hundred-sixty mg of each sample were carefully weighed as quickly as possible to prevent moisture uptake. Samples were then placed in 2 oz sample bottles, into which were placed approximately 27 g of 5 mm glass catalyst beads and 40 ml of reagent dye. Forty-seven sample bottles and a standard check sample were then placed in a Udy batch shaker, and agitated 1.5 hrs. After each group of samples had been agitated, they were placed in a Thelco water bath at 25°C for 3 minutes to stabilize the temperature and allow the particles to settle.

Procedures for calibrating and operating the Udy color analyzer were followed as outlined in the equipment instruction booklet (88). The meter reading on the color analyzer was noted as each sample was decanted into a filter assembly placed in the cuvet of the analyzer. The protein of each sample was then determined by using a soybean protein conversion table supplied with the equipment. The color analyzer was periodically recalibrated using the reference dye.

Computer Analysis of Data

The data were recorded on IBM code sheets and processed through the L.S.U. Computer Research Center by the Department of Experimental Statistics. All selected characters included in this study were adjusted by the computer for competitive or noncompetitive effects. The protein content of all samples were additionally adjusted to the mean of the standard check sample. After the adjustments, an analysis of variance was conducted on each selected character to determine whether significant differences occurred among the progeny and parental lines. Duncan's New Multiple Range test was applied to each character and significant differences among parental lines and progeny for the different characters were reported at the .05 level of probability.

Correlation coefficients were calculated for the following: 1) between all selected characters included in both the F_1 and F_2 portion of this study, which also included the data from the parental lines, 2) between protein percentages obtained for the parental lines grown with the F_1 progeny and those grown with the F_2 progeny as determined by the Udy Dye Method, and 3) between three methods of determining protein for 100 selected samples from which Udy, Kjeldahl, and Infrared protein determinations were made.

Other Calculations

Frequency distributions were prepared to show the relationship between each F_2 progeny and its parents for protein percentages. Broad sense heritability was calculated for each of the selected characters using the formula:

$$H_b = \frac{s^2_{F_2} \sqrt{s^2_{P_1} \cdot s^2_{P_2}}}{s^2_{F_2}}$$

where $s^2_{F_2}$ = total variance (genotypic + environment), and $s^2_{P_1}$ and $s^2_{P_2}$ = estimates of environmental variance (57). The expected genetic advance was estimated for percent protein according to Allard (2) as follows: Gs = (k) (σ_A) (H_b) where Gs = expectation of genetic advance under selection, (k) = 1.76, the 10% selection differential, (σ_A) = phenotypic standard deviation, and (H_b) heritability. The predicted means of each F_2 progeny were determined for protein content by adding the progeny mean and the expected genetic advance. The t test was used to determine if the F_2 protein mean was significantly different from the midparent mean.

RESULTS AND DISCUSSION

Throughout the presentation of this portion of this dissertation, reference to protein content of any of the parents or generations, will refer to protein content obtained by the Udy Dye Method unless otherwise specified.

Parental Lines

The protein content of the parental lines grown with the F_2 population was higher than when they were grown with the F_1 population. However, a highly significant correlation coefficient of .90 was obtained between the mean protein content of the parents grown with the F_1 and F_2 generation. One reason for the difference in the parents may possibly have been due to herbicide damage which was sustained by the F_1 portion of the test. The F_1's and parents were planted at a lower elevation in the field than were the F_2 and parents. The damage occurred early in the growing season when a heavy rain flooded the F_1 test. Linuron had been applied a few days before the rain. Also, corn had been planted the year before, and some of this damage may have been caused by the residual effects of atrazine.

The parents grown with each generation were therefore used with their respective generation for all comparisons and determinations. One set of crosses which involved the line D69-0263, were excluded from the F_1 portion of this study because of too many missing plots.

Although the parental lines grown with the F_1's differed in protein content, only one differed significantly (Table 2). F66-698

Table 2. Mean percent protein, maturity date, plant height, flowering date and height of lower pod for 9 soybean lines and their respective F_1 populations grown on Olivier silt loam, Baton Rouge, 1973.

Parent and cross combinations	Protein %	Maturity date[1]	Plant height[2]	Flowering date[3]	Height of lower pod[2]
D67-6117 x F66-698	45.98 a[4]	59.04 bcd	64.46 def	29.32 defg	13.13 ab
D67-6117 x Tracy	45.94 a	61.43 bcde	70.69 abcde	22.28 bcd	9.79 ab
D67-6117 x Ransom	45.54 a	58.02 bcd	57.03 def	26.33 bcdefg	10.56 ab
D67-6117 x Hutton	45.32 ab	62.82 bcde	73.43 abcde	27.21 cdefg	12.85 ab
D67-6117 x F67-3673	45.31 ab	61.56 bcde	73.74 abcde	25.37 bcdefg	16.94 a
D67-6117 x Pickett 71	44.95 ab	62.77 bcde	62.58 def	27.68 cdefg	11.96 ab
D67-6117 x Bragg	44.60 ab	63.02 bcde	73.15 abcde	24.27 bcde	13.92 ab
D68-4641 x F66-698	46.68 a	62.50 bcde	77.25 abcde	26.50 bcdefg	9.00 ab
D68-4641 x F67-3673	46.47 a	63.35 bcde	63.16 def	19.74 bcd	11.26 ab
D68-4641 x D67-6117	45.46 ab	49.11 b	54.68 def	28.14 bcdefg	18.05 a
D68-4641 x Hutton	45.14 ab	60.11 bcde	72.68 abcde	17.64 bcd	13.32 ab
D68-4641 x Pickett 71	44.85 ab	59.06 bcde	59.84 def	16.08 bc	11.52 ab
D68-4641 x Bragg	43.64 abc	61.61 bcde	74.30 abcde	19.64 bcd	13.17 ab
D68-4641 x Tracy	43.00 abcd	53.30 b	66.63 cdef	14.38 b	11.19 ab
D68-4641 x Ransom	42.93 abcd	52.64 b	56.14 def	15.61 b	11.22 ab
F67-3673 x F66-698	46.24 a	64.38 bcde	89.27 a	34.02 g	14.32 a
F67-3673 x Tracy	45.22 ab	66.56 cde	82.68 abc	24.69 bcde	14.71 a
F67-3673 x Hutton	44.54 ab	66.65 cde	86.31 ab	27.56 cdefg	14.56 a
F67-3673 x Ransom	43.93 ab	68.08 e	70.12 abcde	25.96 bcdefg	11.87 ab
F67-3673 x Bragg	43.90 ab	63.92 bcde	76.19 abcde	30.68 defg	14.02 ab
F67-3673 x Pickett 71	43.87 ab	66.41 cde	76.11 abcde	28.67 defg	11.32 ab
F66-698 x Tracy	45.46 a	58.61 bcd	76.08 abcde	25.30 bcdef	12.01 ab
F66-698 x Ransom	45.24 ab	67.09 de	75.51 abcde	31.15 defg	9.90 ab
F66-698 x Bragg	44.40 ab	65.27 cde	78.88 abcd	34.43 g	9.95 ab
F66-698 x Pickett 71	44.25 ab	59.74 bcde	73.37 abcde	32.76 efg	12.53 ab
F66-698 x Hutton	44.13 ab	63.26 bcde	76.98 abcde	33.88 g	13.99 ab
Tracy x Pickett 71	42.34 bcd	59.07 bcde	70.76 abcde	24.98 bcdef	10.52 ab

(Continued)

Table 2. Continued

Parent and cross combinations	Protein %	Maturity date[1]	Plant height[2]	Flowering date[3]	Height of lower pod[2]
Tracy x Bragg	41.91 bcd	61.05 bcde	67.04 cdef	23.99 bcde	14.84 a
Tracy x Hutton	41.07 bcd	60.50 bcde	65.75 def	31.50 defg	10.50 ab
Tracy x Ransom	41.68 bcd	59.07 bcde	59.12 f	21.76 bcde	12.58 ab
Pickett 71 x Hutton	41.92 bcd	66.82 de	75.59 abcde	27.33 cdefg	11.36 ab
Pickett 71 x Ransom	40.64 cd	65.96 cde	57.76 def	22.98 bcd	10.60 ab
Bragg x Hutton	41.06 bcd	64.44 bcde	69.43 abcdef	28.64 defg	17.80 a
Bragg x Pickett 71	40.13 d	61.31 bcde	58.46 def	27.32 cdefg	10.97 ab
Bragg x Ransom	40.12 d	66.73 cde	65.85 cdef	24.22 bcde	11.12 ab
Hutton x Ransom	40.59 cd	65.75 cde	67.38 bcdef	28.75 defg	12.63 ab
F66-698	46.66 a	56.55 bc	74.98 abcde	33.19 fg	12.17 ab
F67-3673	45.03 ab	65.89 cde	84.21 abc	29.19 defg	15.32 a
D67-6117	44.90 ab	54.33 b	55.58 def	24.86 bcde	12.61 ab
D68-4641	44.35 ab	28.33 a	52.28 ef	6.86 a	11.43 ab
Hutton	42.60 bcd	60.78 bcde	79.01 abcd	30.19 defg	13.83 ab
Pickett 71	42.25 bcd	59.22 bcde	54.51 ef	25.52 bcdefg	10.51 ab
Tracy	41.59 bcd	59.55 bcde	62.90 def	19.19 bcd	11.21 ab
Bragg	41.17 bcd	60.33 bcde	75.78 abcde	23.64 bcd	13.22 ab
Ransom	41.12 bcd	66.89 de	66.80 cdef	22.75 bcd	11.65 ab

[1]Mean maturity days after September 1.
[2]Plant height and height of lower pod means in cm.
[3]Mean flowering days after July 1.
[4]Means within a column followed by a letter in common are not significantly different at the 5% probability level according to Duncan's New Multiple Range Test.

was significantly higher in mean protein content than Hutton, Pickett 71, Tracy, Bragg, and Ransom.

There were significant differences in maturity among the parental lines grown with the F_1's, as expected. D68-4641 was significantly earlier in maturity than all the other parental lines. Its mean maturity date was September 28, 1973. D67-6117 was significantly earlier than F67-3673 and Ransom. D67-6117 had a mean maturity date of October 24, 1973. It was however, not significantly different from the other parental lines (Table 2). F66-698 was significantly earlier maturing than Ransom. Its mean maturity date was October 26, 1973. Other parental lines in this study were not significantly different for maturity date.

Significant differences occurred for plant height among parental lines grown with the F_1's. F67-3673 was significantly taller than was D67-6117, Tracy, Pickett 71, and D67-4641, but not when compared to F66-698, Hutton, Bragg, or Ransom. Hutton was only significantly taller than D68-4641 and Pickett 71. The coefficient of variation for the plant height means was 15.80%.

Both flowering date means and height of lower pod means of the parent lines grown with the F_1's had large coefficients of variation being 24.32% and 30.37%, respectively. Significant differences occurred among the lines as presented in Table 2. D68-4641, the earliest to mature, was also the first to bloom.

F_1 Progeny

The F_1 progeny will be discussed under the headings of the selected characters included in this study.

Protein Content Means

Thirty-six cross combinations were grown with the number of F_1 plants ranging from 2 to 17 per cross. Within each group of crosses having the same female parent, there were no significant differences in protein content means (Table 2). However, there were significant differences for protein content means when comparing F_1 progeny with different female parents. The letter(s) following the female parent shown below comes from Table 2. Three of the F_1 progeny of D67-6117(a), two of D68-4641(a), one of F67-3673(a), and one of F66-698(a) had significantly higher protein means than did those F_1 progeny of Tracy(bcd), Pickett 71(bcd,cd), Bragg(bcd,d), and Hutton(cd) (Table 2). Also four other F_1 progeny of D67-6117(ab), three of D68-4641(ab), five of F67-3673(ab), and four of F66-698(ab) also had significantly higher protein content means than did two F_1 progeny of Bragg(d), one of Hutton(cd), and one of Pickett 71(cd). One F_1 progeny of D68-4641(abc) had significantly higher protein means than did two F_1 progeny of Bragg(d). There were no other significant differences among protein content means of the F_1 progeny.

There was a tendency in all crosses, except one, for the F_1 progeny to vary from the midparent mean usually toward the high protein parent (Table 3). The mean protein content of the F_1 of D68-4641 x Tracy exceeded its midparent mean by only .03%. Twenty-seven means or 75% of the F_1 progeny protein means exceeded their respective midparent mean in protein content. Thirteen means or 36% of the F_1 progeny exceeded their respective high protein parent. This is a higher percentage of F_1's exceeding the midparent and/or high protein parent than was found by Singh and Hadley (74) and Weber et al. (91).

Table 3. Mean percent protein and variance (in parenthesis) of parental lines, the midparent, and F_1 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D67-6117 x	F66-698	44.90 (1.37)	46.66 (1.20)	45.78	45.98[b] (1.17)	.20
D67-6117 x	Tracy	44.90 (1.37)	41.59 (2.21)	43.25	45.94[cd] (0.55)	2.69
D67-6117 x	Ransom	44.90 (1.37)	41.12 (5.02)	43.01	45.54[cd] (2.86)	2.53
D67-6117 x	Hutton	44.90 (1.37)	42.60 (3.13)	43.75	45.32[cd] (0.57)	1.57
D67-6117 x	F67-3673	44.90 (1.37)	45.03 (2.23)	44.97	45.31[bd] (1.36)	.34
D67-6117 x	Pickett 71	44.90 (1.37)	42.25 (3.04)	43.58	44.95[cd] (1.84)	1.37
D67-6117 x	Bragg	44.90 (1.37)	41.17 (4.30)	43.04	44.60[c] (2.44)	1.56
D68-4641 x	F66-698	44.35 (4.81)	46.66 (1.20)	45.51	46.68[bd] (3.54)	1.68
D68-4641 x	F67-3673	44.35 (4.81)	45.03 (2.23)	44.69	46.47[bd] (4.78)	1.78
D68-4641 x	D67-6117	44.35 (4.81)	44.90 (1.37)	44.63	45.46[bd] (5.18)	.83
D68-4641 x	Hutton	44.35 (4.81)	42.60 (3.13)	43.48	45.14[cd] (1.43)	1.66
D68-4641 x	Pickett 71	44.35 (4.81)	42.25 (3.04)	43.30	44.85[cd] (1.31)	1.21
D68-4641 x	Bragg	44.35 (4.81)	41.17 (4.30)	42.76	43.64[c] (0.99)	.88
D68-4641 x	Tracy	44.35 (4.81)	41.59 (2.21)	42.97	43.00[c] (1.21)	.03
D68-4641 x	Ransom	44.35 (4.81)	41.12 (5.02)	42.74	42.93[c] (2.72)	.19

(Continued)

Table 3. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
F67-3673 x	F66-698	45.03 (2.23)	46.66 (1.20)	45.85	46.24[b] (0.90)	.39
F67-3673 x	Tracy	45.03 (2.23)	41.59 (2.21)	43.31	45.22[cd] (2.02)	1.91
F67-3673 x	Hutton	45.03 (2.23)	42.60 (3.13)	43.82	44.54[c] (0.82)	.72
F67-3673 x	Ransom	45.03 (2.23)	41.12 (5.02)	43.08	43.93[c] (0.91)	.85
F67-3673 x	Bragg	45.03 (2.23)	41.17 (3.04)	43.10	43.90[c] (1.37)	.23
F66-698 x	Tracy	46.66 (1.20)	41.59 (2.21)	44.13	45.46[c] (1.19)	1.33
F66-698 x	Ransom	46.66 (1.20)	41.12 (5.02)	43.89	45.24[c] (2.55)	1.35
F66-698 x	Bragg	46.66 (1.20)	41.17 (4.30)	43.92	44.40[c] (1.64)	.48
F66-698 x	Pickett 71	46.66 (1.20)	42.25 (3.04)	44.46	44.25[b] (2.71)	- .21
F66-698 x	Hutton	46.66 (1.20)	42.60 (3.13)	44.63	44.13[b] (2.38)	- .50
Tracy x	Pickett 71	41.59 (2.21)	42.25 (3.04)	41.90	42.34[b] (2.21)	.42
Tracy x	Bragg	41.59 (2.21)	41.17 (4.93)	41.38	41.91[cd] (0.39)	.53
Tracy x	Ransom	41.59 (2.21)	41.12 (5.02)	41.36	41.68[cd] (3.33)	.32
Tracy x	Hutton	41.59 (2.21)	42.60 (3.13)	42.10	41.07[ce] (8.70)	-1.03
Pickett x	Hutton	42.25 (3.04)	42.60 (3.13)	42.43	41.92[ce] (8.39)	- .49

(Continued)

Table 3. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
Pickett x Ransom		42.25 (3.04)	41.12 (5.02)	41.69	40.64[be] (1.14)	-1.05
Bragg x Hutton		41.17 (4.93)	42.60 (3.13)	41.89	41.06[ce] (2.56)	- .83
Bragg x Pickett 71		41.17 (4.93)	42.25 (3.04)	41.71	40.13[ce] (1.84)	-1.58
Bragg x Ransom		41.17 (4.93)	41.12 (5.02)	41.15	40.12[be] (0.33)	-1.03
Hutton x Ransom		42.60 (3.13)	41.12 (5.02)	41.85	40.59[be] (0.92)	-1.25

[a] Coefficient of variation for all protein means 2.56%.
[b] F_1 more like male parent in protein content.
[c] F_1 more like female parent in protein content.
[d] Exceeds highest parent in protein content.
[e] Less than low parent in protein content.

Heterosis for protein for the 13 F_1 progeny averaged .49% protein or about 1% above the high parent. However, the F_1 of D67-6117 x Tracy and D68-4641 x Hutton had relatively good specific combining ability, exceeding the high parent by 1.05 and .79% protein, respectively. D67-6117 was the best parent for general combining ability with six of the eight F_1 crosses with it exceeding the high parent. D68-4641 also had good general combining ability with five of the eight cross combinations exceeding the high parent.

Nine means or 25% of the F_1 progeny protein means were less than their midparent. Seven means or 19% of the F_1 progeny contained less protein than their respective low parent. Each of these F_1 progeny means were derived from low protein x low protein parents, with Pickett 71 and Bragg as one of the parents in three of the seven crosses. The F_1 of Pickett 71 x Bragg was 1.04% lower in protein than the low parent.

These data indicates that other than additive gene action was involved in protein content of the F_1 progeny. Other researchers have observed dominance and epistatic variance effects in protein, but to a smaller degree than the additive effect (10, 31, 32, 38). Strong maternal effects and cytoplasmatic effects were reported in soybeans by Singh and Hadley (74). This may have caused the F_1 progeny to be skewed toward the high protein parent, since the high protein parent was used as the female in most crosses. The variance of most of the F_1 progeny were lower than that of one or both parents.

Generally, the data in Table 3 indicate that there was a tendency for the F_1 progeny to be higher in protein than their respective midparent mean when either two high protein lines or a high and a medium

protein line were crossed. There also was a general tendency for the F_1 progeny to be lower in protein content than its respective midparent mean when two low protein lines were crossed. The protein content means for all the F_1 progeny included in this study ranged from a low of 40.13% for Bragg x Pickett 71 to a high of 46.68% for D68-4641 x F66-698. The overall coefficient of variation for mean protein content of the parents and F_1 progeny was 2.56%.

Maturity Date Means

There were no significant differences among maturity date means of the F_1 progeny having the same female parent (Table 2). However, there were significant differences among some of the F_1 progeny when comparing F_1's with different female parents. Three of the F_1 progeny having D68-4641(b) as the female parent had significantly earlier maturity date means than did four of the F_1 progeny of F67-3673(cde,e), two of the F_1's of F66-698(cde,de), two of the F_1's of Pickett 71(cde, de), one of the F_1's of Bragg(cde), and the F_1 of Hutton(cde). The maturity dates means of the significantly earlier maturing F_1 progeny of D68-4641 range from October 19, 1973 to October 23, 1973. Two F_1 progeny of D67-6117(bcd) and one of F66-698(bcd) were significantly earlier maturing than one of the F_1 progeny of F67-3673(e). There were no other significant differences among the F_1 progeny having different female parents.

When comparing the midparent means to the F_1 progeny means as shown in Table 4, all crosses except four deviated from the midparent means by at least one day. The mean maturity date of the F_1's of F67-3673 x Bragg, F66-698 x Tracy, Tracy x Pickett 71, and Tracy x

Table 4. Mean maturity date (after September 1) and variance (in parenthesis) of parental lines, the midparent, and F_1 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D67-6117 x	F66-698	54.33 (16.44)	56.55 (164.03)	55.44	59.04[bc] (0.01)	3.60
D67-6117 x	Tracy	54.33 (16.44)	59.55 (49.28)	56.94	61.43[bc] (11.98)	4.49
D67-6117 x	Ransom	54.33 (16.44)	66.89 (4.19)	60.61	58.02[d] (34.50)	- 2.59
D67-6117 x	Hutton	54.33 (16.44)	60.78 (170.50)	57.56	62.82[bc] (25.34)	5.26
D67-6117 x	F67-3673	54.33 (16.44)	65.89 (9.19)	60.11	61.56[b] (21.33)	1.45
D67-6117 x	Pickett 71	54.33 (16.44)	59.22 (0.11)	56.78	62.77[bc] (11.12)	5.99
D67-6117 x	Bragg	54.33 (16.44)	60.33 (137.69)	57.33	63.02[bc] (9.59)	6.36
D68-4641 x	F66-698	28.33 (62.69)	56.55 (164.03)	42.44	62.50[bc] (26.06)	20.06
D68-4641 x	F67-3673	28.33 (62.69	65.89 (9.19)	47.10	63.35[b] (67.29)	16.25
D68-4641 x	D67-6117	28.33 (62.69)	54.33 (16.44)	41.33	49.11[b] (722.00)	7.78
D68-4641 x	Hutton	28.33 (62.69)	60.78 (170.50)	44.56	60.11[b] (4.00)	15.55
D68-4641 x	Pickett 71	28.33 (62.69)	59.22 (0.11)	43.78	59.06[b] (0.01)	15.28
D68-4641 x	Bragg	28.33 (62.69)	60.33 (137.69)	44.33	61.61[bc] (8.33)	17.28
D68-4641 x	Tracy	28.33 (62.69)	59.55 (49.28)	43.94	53.30[b] (19.80)	9.36

(Continued)

Table 4. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D68-4641 x	Ransom	28.33 (62.69)	66.89 (4.19)	47.61	52.64[b] (8.08)	5.03
F67-3673 x	F66-698	65.89 (9.19)	56.55 (164.03)	61.22	64.38[d] (17.12)	3.16
F67-3673 x	Tracy	65.89 (9.19)	59.55 (49.28)	62.72	66.56[cd] (7.03)	3.84
F67-3673 x	Hutton	65.89 (9.19)	60.78 (170.50)	63.34	66.65[cd] (4.77)	3.31
F67-3673 x	Ransom	65.89 (9.19)	66.89 (4.19)	66.36	68.08[bc] (0.01)	1.69
F67-3673 x	Bragg	65.89 (9.19)	60.33 (137.69)	63.11	63.92[b] (2.21)	.81
F67-3673 x	Pickett 71	65.89 (9.19)	59.22 (0.11)	62.56	66.41[cd] (6.82)	3.85
F66-698 x	Tracy	56.55 (164.03)	59.55 (49.28)	58.05	58.61[b] (3.00)	.56
F66-698 x	Ransom	56.55 (164.03)	66.89 (4.19)	61.22	67.09[bc] (0.00)	5.37
F66-698 x	Bragg	56.55 (164.03)	60.33 (137.69)	58.44	65.27[bc] (11.35)	6.83
F66-698 x	Pickett 71	56.55 (164.03)	59.22 (0.11)	57.89	59.74[bc] (38.73)	1.85
F66-698 x	Hutton	56.55 (164.03)	60.78 (170.50)	58.67	63.26[bc] (11.13)	4.59
Tracy x	Pickett 71	59.55 (49.28)	59.22 (0.11)	59.39	59.07[b] (0.01)	- .32
Tracy x	Bragg	59.55 (49.28)	60.33 (137.69)	59.94	61.05[bc] (11.97)	1.11
Tracy x	Ransom	59.55 (49.28)	66.89 (4.19)	63.22	59.07[de] (58.19)	- 4.15

(Continued)

Table 4. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
Tracy	Hutton	59.55 (49.28)	60.78 (170.50)	60.17	60.50[b] (3.86)	.33
Pickett 71	Hutton	59.22 (0.11)	60.78 (170.50)	60.00	66.82[bc] (2.89)	6.82
Pickett 71	Ransom	59.22 (0.11)	66.89 (4.19)	63.06	65.96[b] (6.51)	2.90
Bragg	Hutton	60.33 (137.69)	60.78 (170.50)	60.56	64.44[bc] (16.33)	3.88
Bragg	Pickett 71	60.33 (137.69)	59.22 (0.11)	59.72	61.31[cd] (20.59)	1.53
Bragg	Ransom	60.33 (137.69)	66.89 (4.19)	63.61	66.73[b] (1.34)	3.12
Hutton	Ransom	6o.78	66.89 (170.50)	63.84 (4.19)	65.75[b]	1.91 (23.22)

[a]Coefficient of variation of all maturity date means 9.83%.
[b]F_1 more like male parent in maturity date.
[c]F_1 more like female parent in maturity date.
[d]Later maturing than the latest maturing parent.
[e]Earlier maturing than the earliest maturing parent.

Hutton were the same as their respective midparent maturity date. Thirty means, or 83% of the F_1 progeny means exceeded their respective midparent mean and tended to be more like the later maturing parent. This was generally in agreement with work by Weber et al. (91). Nineteen means, or 53% of the F_1 progeny means had later maturity date means than their respective later maturing parent. Two means, or 6% of the F_1 progeny means were less than their respective midparent maturity dates. The F_1 progeny of Tracy x Ransom had the same mean maturity date as its earlier maturing parent, Tracy. Generally, the data in Table 4 indicated that there was a tendency for the F_1 progeny to be later maturing than the respective later maturing parent. Ransom was the male parent in the two cases where the progeny were more like the earlier maturing parent (D67-6117 x Ransom, and Tracy x Ransom). Heterosis for maturity date as an average of the F_1 progeny exceeding the late parent was about two days. The maturity dates means of all the F_1 progeny ranged from an early mean maturity date of October 25, 1973 which occurred for the F_1 progeny of Bragg x Pickett 71, to a late maturity date mean of November 5, 1973, which occurred for the F_1 progeny of F67-3673 x Ransom. The overall coefficient of variation for maturity date means of the parents and F_1 progeny was 9.83%.

Plant Height Means

There were significant differences for plant height means among F_1 progeny having different female parents. The F_1 progeny of F67-3673 x F66-698(a) and F67-3673 x Hutton(ab) were significantly taller than three of the F_1 progeny of D67-6117(def), five of D68-4641(cdef,def), three of Tracy(cdef,def,f), one of Pickett 71(def), and two of

Bragg(cdef,def). Only the F_1 progeny of F67-3673 x F66-698(a) were significantly taller than the F_1 progeny of Hutton x Ransom(bcdef). The F_1 progeny of F67-3673 x Tracy(abc) were significantly taller than three F_1 progeny of D67-6117(def), four of D68-4641(def), two of Tracy(def,f), one of Pickett 71(def), and one of Bragg(def). There were no other significant differences among the F_1 progeny for plant height.

In comparing the midparent means to the F_1 progeny plant height means as shown in Table 5, there was a tendency in all crosses except three to vary from their respective midparent means by more than 2 cm. The plant height means of the F_1 progeny of D67-6117 x F66-698, D68-4641 x D67-6117, and F66-698 x Hutton were close to their midparent mean for plant height. Twenty means or 56% of the F_1 progeny means exceeded their respective midparent mean in plant height being more like the taller parent. Ten means or 28% of the F_1 progeny were taller than their respective tallest parent. Heterosis for plant height for the 10 F_1 progeny averaged 4.20%. This is a lower percentage than reported by Brim and Cockerham (10) but close to that reported by Weber et al. (91). The F_1 of Tracy x Pickett 71 and D67-6117 x Tracy had relatively good specific combining ability, exceeding the tallest parent by 7.86 and 7.79 cm, respectively. Thirteen means or 34% of the F_1 progeny means were less than their respective midparent mean. Four means or 11% of the F_1 progeny means were shorter than their respective shorter parent. This data seems to indicate that other than additive gene action was involved in plant height of the F_1 progeny (38).

The plant height means of all F_1 progeny ranged from a low of 54.68 cm for D68-4641 x D67-6117 to a high of 89.27 cm for F67-3673 x

Table 5. Mean plant height (in cm) and variance (in parenthesis) of parental lines, the midparent, and F_1 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D67-6117 x	F66-698	55.58 (48.48)	74.98 (85.24)	65.28	64.46[b] (198.13)	- .82
D67-6117 x	Tracy	55.58 (48.48)	62.90 (60.09)	59.24	70.69[cd] (11.98)	11.45
D67-6117 x	Ransom	55.58 (48.48)	66.80 (66.15)	61.19	57.03[c] (114.31)	4.16
D67-6117 x	Hutton	55.58 (48.48)	79.01 (146.62)	67.30	73.43[c] (34.84)	6.13
D67-6117 x	F67-3673	55.58 (48.48)	84.21 (60.36)	69.90	73.74[c] (140.33)	3.84
D67-6117 x	Pickett 71	55.58 (48.48)	54.51 (12.73)	55.05	62.58[bd] (69.74)	7.53
D67-6117 x	Bragg	55.58 (48.48)	75.78 (113.35)	65.68	73.15[c] (52.18)	7.47
D68-4641 x	F66-698	52.28 (56.33)	74.98 (85.24)	63.63	77.25[cd] (122.46)	13.62
D68-4641 x	F67-3673	52.28 (56.33)	84.21 (60.36)	68.25	63.16[b] (55.44)	- 5.09
D68-4641 x	D67-6117	52.28 (56.33)	55.58 (48.48)	53.93	54.68[c] (465.13)	.75
D68-4641 x	Hutton	52.28 (56.33)	79.01 (146.62)	65.65	72.68[c] (9.58)	7.03
D68-4641 x	Pickett 71	52.28 (56.33)	54.51 (12.73)	53.40	59.84[cd] (65.55)	6.44
D68-4641 x	Bragg	52.28 (56.33)	75.78 (43.35)	64.03	74.30[c] (3.23)	10.27
D68-4641 x	Tracy	52.28 (56.33)	62.90 (60.09)	57.59	66.63[cd] (68.36)	9.04

(Continued)

Table 5. Continued

Cross combinations Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D68-4641 x	Ransom	52.28 (56.33)	66.80 (66.15)	59.54	56.14[b] (68.95)	- 3.40
F67-3673 x	F66-698	84.21 (60.36)	74.98 (85.24)	79.60	89.27[bd] (108.37)	9.67
F67-3673 x	Tracy	84.21 (60.36)	62.90 (60.09)	73.56	82.68[b] (269.09)	9.12
F67-3673 x	Hutton	84.21 (60.36)	79.01 (146.62)	81.61	86.31[bd] (52.30)	4.70
F67-3673 x	Ransom	84.21 (60.36)	66.80 (66.15)	75.51	70.12[c] (128.69)	- 5.39
F67-3673 x	Bragg	84.21 (60.36)	75.78 (43.35)	80.00	76.19[c] (198.62)	- 3.81
F67-3673 x	Pickett 71	84.21 (60.36)	54.51 (12.73)	69.36	76.11[b] (61.92)	6.75
F66-698 x	Tracy	74.98 (85.24)	62.90 (60.09)	68.94	76.08[c] (28.36)	7.14
F66-698 x	Ransom	74.98 (85.24)	66.80 (66.15)	70.89	75.51[bd] (149.59)	4.62
F66-698 x	Bragg	74.98 (85.24)	75.78 (43.35)	75.38	78.88[cd] (153.77)	3.50
F66-698 x	Pickett 71	74.98 (85.24)	54.51 (12.73)	64.75	73.37[b] (151.60)	8.62
F66-698 x	Hutton	74.98 (85.24)	79.01 (146.62)	77.00	76.98[b] (53.06)	- .02
Tracy x	Pickett 71	62.90 (60.09)	54.51 (12.73)	58.71	70.76[bd] (251.90)	12.05
Tracy x	Bragg	62.90 (60.09)	75.78 (43.35)	69.34	67.04[b] (412.39)	- 2.30
Tracy x	Ransom	62.90 (60.09)	66.80 (66.15)	64.85	59.12[be] (111.04)	- 5.73

(Continued)

Table 5. Continued

Cross combinations Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
Tracy	Hutton	62.90 (60.09)	79.01 (146.62)	70.96	65.75[b] (137.53)	- 5.21
Pickett 71	Hutton	54.51 (12.73)	79.01 (146.62)	66.76	75.59[c] (76.09)	8.83
Pickett 71	Ransom	54.51 (12.73)	66.80 (66.15)	60.66	57.76[b] (13.25)	- 2.90
Bragg	Hutton	75.78 (43.35)	79.01 (146.62)	77.40	69.43[be] (230.25)	- 7.97
Bragg	Pickett 71	75.78 (43.35)	54.51 (12.73)	65.15	58.46[c] (246.76)	- 6.69
Bragg	Ransom	75.78 (43.35)	66.80 (66.15)	71.29	65.85[ce] (20.79)	- 5.44
Hutton	Ransom	79.01 (146.62)	66.80 (66.15)	72.91	67.38[c] (12.53)	- 5.53

[a]Coefficient of variation of all plant height means 15.80%.
[b]F_1 more like female parent in plant height.
[c]F_1 more like male parent in plant height.
[d]F_1 taller than tallest parent.
[e]F_1 shorter than shortest parent.

F66-698. The overall coefficient of variation for plant height means of the parents and F_1 progeny was 15.80%.

Flowering Date and Height of Lower Pod Means

Significant differences among F_1 progeny for flowering date and height of lower pod means are presented in Table 2. Comparisons of F_1 means to their respective midparent means are presented in Tables 6 and 7 for these characters. The coefficients of variation for flowering date and plant height means of all F_1 combinations were 24.32% and 30.37%, respectively.

The phenotypic correlation coefficients between all combinations of characters studied for the parents and F_1 populations are presented in Table 8. Protein and the characters flowering date, plant height, and height of the lower pod were all positively correlated and highly significant, but the associations were low. Maturity date and the characters flowering date, plant height, height of lower pod, and yield were all positive, highly significant and were moderate, moderately low, low and low in association, respectively. Plant height and the characters flowering date, height of lower pod, and yield, were moderate, low, and low in association, respectively. Height of lower pod and flowering date, was positive and highly significant, but the association was low. A low negative but highly significant correlation occurred between height of lower pods and yield. All other correlations, yield and flowering date, protein and maturity date, and protein and yield were not significant.

Table 6. Mean flowering date (after July 1) and variance (in parenthesis) of parental lines, the midparent, and F_1 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D67-6117 x	F66-698	24.86 (2.19)	33.19 (63.53)	29.03	29.32[b] (10.72)	.29
D67-6117 x	Tracy	24.86 (2.19)	19.19 (1.03)	22.03	22.28[c] (4.60)	.25
D67-6117 x	Ransom	24.86 (2.19)	22.75 (3.36)	23.81	26.33[c] (30.76)	2.52
D67-6117 x	Hutton	24.86 (2.19)	30.19 (10.28)	27.53	27.21[c] (14.02)	- .32
D67-6117 x	F67-3673	24.86 (2.19)	29.19 (8.53)	27.03	25.37[c] (7.00)	-1.66
D67-6117 x	Pickett 71	24.86 (2.19)	25.52 (0.61)	25.19	27.68[bd] (47.91)	2.49
D67-6117 x	Bragg	24.86 (2.19)	23.64 (3.00)	24.25	24.27[c] (24.38)	.02
D68-4641 x	F66-698	6.86 (25.44)	33.19 (63.53)	20.03	26.50[b] (6.96)	6.46
D68-4641 x	F67-3673	6.86 (25.44)	29.19 (8.53)	18.03	19.74[b] (18.32)	1.71
D68-4641 x	D67-6117	6.86 (25.44)	24.86 (2.19)	15.86	28.14[bd] (264.50)	12.28
D68-4641 x	Hutton	6.86 (25.44)	30.19 (10.28)	18.54	17.64[c] (0.00)	- .90
D68-4641 x	Pickett 71	6.86 (25.44)	25.52 (0.61)	16.19	16.07[c] (7.47)	- .12
D68-4641 x	Bragg	6.86 (25.44)	23.64 (3.00)	15.25	19.64[b] (0.00)	4.39
D68-4641 x	Tracy	6.86 (25.44)	19.19 (1.03)	13.03	14.38[b] (5.13)	1.35

(Continued)

Table 6. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D68-4641 x Ransom		6.86 (25.44)	22.75 (3.36)	14.81	15.61[b] (10.00)	.80
F67-3673 x F66-698		29.19 (8.53)	33.19 (63.53)	31.19	34.02[bd] (6.61)	2.83
F67-3673 x Tracy		29.19 (8.53)	19.19 (1.03)	24.19	24.69[c] (5.57)	.50
F67-3673 x Hutton		29.19 (8.53)	30.19 (10.28)	29.69	27.56[ce] (11.41)	-2.13
F67-3673 x Ransom		29.19 (8.53)	22.75 (3.36)	25.97	25.96[b] (18.14)	- .01
F67-3673 x Bragg		29.19 (8.53)	23.64 (3.00)	26.42	30.68[cd] (56.63)	4.26
F67-3673 x Pickett 71		29.19 (8.53)	25.52 (0.61)	27.36	28.67[c] (17.06)	1.31
F66-698 x Tracy		33.19 (63.53)	19.19 (1.03)	26.19	25.30[b] (0.79)	- .89
F66-698 x Ransom		33.19 (63.53)	22.75 (3.36)	27.97	31.15[c] (28.27)	3.18
F66-698 x Bragg		33.19 (63.53)	23.64 (3.00)	28.42	34.43[cd] (29.25)	6.01
F66-698 x Pickett 71		33.19 (63.53)	25.52 (0.61)	29.36	32.76[c] (31.95)	3.40
F66-698 x Hutton		33.19 (63.53)	30.19 (10.28)	31.69	33.88[cd] (20.86)	2.19
Tracy x Pickett 71		19.19 (1.03)	25.52 (0.61)	22.36	24.98[b] (24.29)	2.62
Tracy x Bragg		19.19 (1.03)	23.64 (3.00)	21.42	23.99[bd] (27.51)	2.57
Tracy x Ransom		19.19 (1.03)	22.75 (3.36)	20.97	21.76[b] (35.81)	.76

(Continued)

Table 6. Continued

Cross combinations Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
Tracy	Hutton	19.19 (1.03)	30.19 (10.28)	24.64	31.50[bd] (194.64)	6.81
Pickett 71	Hutton	25.52 (0.61)	30.19 (10.28)	27.86	27.33[c] (28.38)	- .53
Pickett 71	Ransom	25.52 (0.61)	22.75 (3.36)	24.14	22.98[b] (16.02)	-1.16
Bragg	Hutton	24.64 (3.00)	30.19 (10.28)	26.92	28.64[b] (7.00)	1.72
Bragg	Pickett 71	24.64 (3.00)	25.52 (0.61)	24.58	27.32[bd] (30.76)	2.74
Bragg	Ransom	24.64 (3.00)	22.75 (3.36)	23.20	24.22[c] (22.74)	1.02
Hutton	Ransom	30.19 (10.28)	22.75 (3.36)	26.47	28.75[b] (82.74)	2.28

[a]Coefficient of variation of all flowering date means 24.32%.
[b]F_1 more like male parent for flowering date.
[c]F_1 more like female parent for flowering date.
[d]Later flowering than the latest flowering parent.
[e]Earlier flowering than the earliest flowering parent.

Table 7. Mean height of lower pods (in cm) and variance (in parenthesis) of parental lines, the midparent, and F_1 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D67-6117 x F66-698		12.61 (10.41)	12.17 (3.32)	12.39	13.13[bd] (19.05)	.74
D67-117 x Tracy		12.61 (10.41)	11.21 (3.71)	11.91	9.79[ce] (8.12)	-2.12
D67-117 x Ransom		12.61 (10.41)	11.65 (1.17)	12.13	10.56[ce] (10.67)	-1.57
D67-6117 x Hutton		12.61 (10.41)	13.83 (13.01)	13.22	12.85[b] (9.70)	- .37
D68-6117 x F67-3673		12.61 (10.41)	15.32 (15.02)	13.97	16.94[cd] (4.16)	2.67
D67-6117 x Pickett 71		12.61 (10.41)	10.51 (4.16)	11.56	11.96[b] (14.97)	.40
D67-6117 x Bragg		12.61 (10.41)	13.22 (23.88)	12.92	13.92[cd] (12.66)	1.00
D68-4641 x F66-698		11.43 (4.46)	12.17 (3.32)	11.80	9.00[be] (10.53)	-2.80
D68-4641 x F67-3673		11.43 (4.46)	15.32 (15.02)	13.38	11.26[be] (8.87)	-2.12
D68-4641 x D67-6117		11.43 (4.46)	12.61 (10.41)	12.02	18.05[cd] (3.13)	6.03
D68-4641 x Hutton		11.43 (4.46)	13.83 (13.01)	12.63	13.32[c] (6.07)	.67
D68-4641 x Pickett 71		11.43 (4.46)	10.51 (4.16)	10.97	11.52[bd] (14.83)	.55
D68-4641 x Bragg		11.43 (4.46)	13.22 (23.88)	12.33	13.17[c] (5.73)	.84
D68-4641 x Tracy		11.43 (4.46)	11.21 (3.71)	11.32	11.19[ce] (8.41)	- .13

(Continued)

Table 7. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
D68-4641 x Ransom		11.43 (4.46)	11.65 (1.17)	11.54	11.22[be] (3.50)	- .32
F67-3673 x F66-698		15.32 (15.02)	12.17 (3.32)	13.75	14.32[b] (15.67)	.57
F67-3673 x Tracy		15.32 (15.02)	11.21 (3.71)	13.27	14.71[b] (40.50)	1.44
F67-3673 x Hutton		15.32 (15.02)	13.83 (13.01)	14.58	14.56[c] (21.61)	- .02
F67-3673 x Ransom		15.32 (15.02)	11.65 (1.17)	13.49	11.87[c] (12.85)	-1.62
F67-3673 x Bragg		15.32 (15.02)	13.22 (23.88)	14.27	14.02[c] (39.92)	- .25
F67-3673 x Pickett 71		15.32 (15.02)	10.51 (4.16)	12.92	11.32[c] (16.62)	-1.60
F66-698 x Tracy		12.17 (3.32)	11.21 (3.71)	11.69	12.01[b] (11.89)	.32
F66-698 x Ransom		12.17 (3.32)	11.65 (1.17)	11.91	9.90[ce] (16.10)	-2.01
F66-698 x Bragg		12.17 (3.32)	13.22 (23.88)	12.70	9.95[be] (9.69)	-2.75
F66-698 x Pickett 71		12.17 (3.32)	10.51 (4.16)	11.34	12.53[b] (17.80)	1.19
F66-698 x Hutton		12.17 (3.32)	13.83 (13.01)	13.00	13.99[cd] (15.94)	.99
Tracy x Pickett 71		11.21 (3.71)	10.51 (4.16)	10.86	10.52[c] (22.88)	- .34
Tracy x Bragg		11.21 (3.71)	13.22 (23.88)	12.22	14.84[cd] (32.33)	2.62
Tracy x Ransom		11.21 (3.71)	11.65 (1.17)	11.43	12.58[c] (14.85)	1.15

(Continued)

Table 7. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_1	Difference between F_1 and midparent
Tracy	Hutton	11.21 (3.71)	13.83 (13.01)	12.52	10.50[be] (10.53)	-2.02
Pickett 71	Hutton	10.51 (4.16)	13.83 (13.01)	12.17	11.36[b] (3.95)	- .48
Pickett 71	Ransom	10.51 (4.16)	11.65 (1.17)	11.08	10.60[b] (13.19)	- .48
Bragg	Hutton	13.22 (23.88)	13.83 (13.01)	13.53	17.80[cd] (43.75)	4.25
Bragg	Pickett 71	13.22 (23.88)	10.51 (4.16)	11.87	10.97[c] (12.52)	- .90
Bragg	Ransom	13.22 (23.88)	11.65 (1.17)	12.44	11.12[ce] (11.19)	-1.32
Hutton	Ransom	13.83 (23.88)	11.65 (1.17)	12.74	12.63[c] (2.60)	- .11

[a]Coefficient of variation of all height of lower pod means 30.37%.
[b]F_1 more like female parent for height of lower pod.
[c]F_1 more like male parent for height of lower pod.
[d]Lowest pod higher than highest parent lower pod.
[e]Lowest pod shorter than shortest parent lower pod.

Table 8. Phenotypic correlation coefficients between all selected characters for parents and F_1 populations grown on Olivier silt loam, Baton Rouge, 1973.

Selected characters	Maturity date	Plant height	H.L.P.[1]	Yield	Protein content
Flowering date	.50**	.36**	.18**	-.22	.16**
Maturity date		.30**	.09**	.13**	.02
Plant height			.20**	.11**	.25**
H.L.P.[1]				.08**	.05**
Yield					-.04

**P 0.01

[1]Height of lower pod.

Parent Lines Grown with F_2 Progeny

Several parental lines grown with the F_2 generation differed significantly in protein content as shown in Table 9. F66-698, D67-6117, D69-0263, and F67-3673 were significantly higher in protein content than Pickett 71, Bragg, and Ransom. However, they were not significantly higher in protein content when compared with Tracy, D68-4641, or Hutton. Also Tracy, D68-4641, and Hutton were not significantly higher in protein content when compared with Pickett 71, Bragg, or Ransom.

There was only one parental line, D68-4641, that was significantly earlier maturing than all the others among those grown with the F_2 population. Its mean maturity date was October 5, 1973. However, the coefficient of variation for this line was 14.52% which suggests that this line was not homogeneous.

Only F67-3673 and Hutton were significantly taller than Ransom and D68-4641, the shorter two parents.

Significant differences occurred among flowering date means of some parental lines (Table 9). D68-4641 was significantly earlier flowering than all the other parental lines except Tracy. Tracy was significantly earlier flowering than was F67-3673, D69-0263, and F66-698, but was not different from the other parental lines.

F_2 Progeny

There were no significant differences for protein content means among the different F_2 lines having the same female parent (Table 9). However, there were significant differences among F_2 lines for mean

Table 9. Mean percent protein, maturity date, plant height, flowering date and height of lower pod for 10 soybean lines and their respective F_2 populations grown on Olivier silt loam, Baton Rouge, 1973.

Parent and cross combinations	Protein %	Maturity date[1]	Plant height[2]	Flowering date[3]	Height of lower pod[2]
D69-0263 x F66-698	49.78 a[4]	53.94 abcde	62.20 cde	26.55 bcd	10.99 ab
D69-0263 x D67-6117	49.63 a	56.42 abcdef	67.10 abcde	38.02 fg	10.48 ab
D69-0263 x Tracy	49.12 a	65.88 ef	73.12 abcd	32.41 ef	13.20 a
D69-0263 x F67-3673	47.74 a	55.47 abcde	79.70 ab	32.26 def	12.45 ab
D69-0263 x Hutton	47.17 ab	62.40 cdef	69.87 abcd	30.37 def	9.37 ab
D69-0263 x Bragg	46.96 abc	63.11 def	62.41 cde	31.22 def	9.97 ab
D69-0263 x Pickett 71	46.92 abc	61.78 cdef	62.41 cde	31.34 def	11.03 ab
D69-0263 x Ransom	45.80 abcd	64.52 ef	60.42 cde	29.65 def	10.75 ab
F67-3673 x F66-698	48.89 a	63.97 ef	81.63 ab	38.50 g	10.66 ab
F67-3673 x Tracy	47.87 a	65.89 ef	77.74 abc	28.99 cde	8.68 ab
F67-3673 x Hutton	47.22 ab	64.24 ef	76.11 abc	32.60 ef	12.08 ab
F67-3673 x Ransom	46.75 abc	67.53 ef	69.41 abcd	30.69 def	11.43 ab
F67-3673 x Bragg	46.58 abc	65.83 ef	82.77 a	30.71 def	12.76 ab
F67-3673 x Pickett 71	46.68 abc	65.16 ef	69.06 abcd	31.40 def	10.29 ab
D67-6117 x F66-698	48.86 a	61.78 cdef	67.96 abcd	35.19 f	11.26 ab
D67-6117 x F67-3673	48.70 a	62.81 def	73.67 abcde	30.90 def	13.74 a
D67-6117 x Tracy	47.17 a	56.63 bcdef	67.96 abcd	25.62 bcd	10.30 ab
D67-6117 x Hutton	48.64 a	66.50 ef	66.97 bcde	30.95 def	12.33 ab
D67-6117 x Bragg	47.15 ab	60.21 bcdef	65.10 bcde	30.60 def	12.38 ab
D67-6117 x Pickett 71	46.45 abc	58.77 bcdef	56.14 de	28.21 cde	10.20 ab
D67-6117 x Ransom	46.04 abcd	58.34 bcdef	56.63 de	27.65 bcde	11.48 ab
D68-4641 x F66-698	48.62 a	52.43 abcd	67.33 abcd	25.03 abc	10.89 ab
D68-4641 x F67-3673	48.60 a	52.69 abcd	65.56 bcde	22.04 a	10.24 ab
D68-4641 x D67-6117	48.89 a	40.62 a	54.65 de	20.80 a	9.47 ab
D68-4641 x D69-0263	48.80 a	47.61 ab	62.67 cde	21.86 a	10.66 ab
D68-4641 x Hutton	47.03 ab	55.98 abcde	67.37 abcd	23.06 ab	11.19 ab
D68-4641 x Pickett 71	46.97 abc	50.11 abc	59.17 cde	20.56 a	8.90 ab

(Continued)

Table 9. Continued

Parent and cross combinations	Protein %	Maturity date[1]	Plant height[2]	Flowering date[3]	Height of lower pod[2]
D68-4641 x Bragg	46.64 abc	44.86 a	58.94 cde	20.34 a	9.24 ab
D68-4641 x Tracy	45.49 abcd	43.78 a	60.90 cde	19.71 a	9.33 ab
D68-4641 x Ransom	45.23 abcd	49.57 abc	58.34 cde	20.92 a	8.87 ab
F66-698 x Ransom	49.14 a	60.75 cdef	69.54 abcd	35.19 f	10.53 ab
F66-698 x Hutton	48.31 a	59.41 bcdef	74.59 abcd	34.03 f	10.62 ab
F66-698 x Tracy	47.70 a	60.10 bcdef	72.73 abcd	29.92 def	10.07 ab
F66-698 x Pickett 71	46.43 abc	63.71 def	64.91 cde	32.35 def	11.24 ab
F66-698 x Bragg	46.06 abc	68.40 f	74.73 abcd	34.24 f	12.11 ab
Pickett 71 x Hutton	45.23 abcd	64.32 ef	51.04 e	29.07 cde	11.52 ab
Pickett 71 x Ransom	44.15 cd	60.95 cdef	48.57 e	25.27 abc	7.16 b
Tracy x Pickett 71	45.19 abcd	60.82 cdef	66.20 bcde	26.22 bcd	9.49 ab
Tracy x Hutton	45.64 abcd	60.70 cdef	67.11 abcd	23.99 ab	10.10 ab
Tracy x Bragg	44.88 bcd	61.05 cdef	65.68 bcde	29.72 de	11.57 ab
Tracy x Ransom	44.12 cd	58.31 bcdef	56.09 de	25.37 bcd	9.04 ab
Hutton x Ransom	44.02 cd	66.66 ef	63.64 cde	28.94 cde	9.89 ab
Bragg x Hutton	44.78 bcd	64.20 ef	74.54 abcd	31.57 def	12.46 ab
Bragg x Pickett 71	44.41 bcd	60.24 bcdef	61.08 cde	27.92 bcde	8.49 ab
Bragg x Ransom	44.22 cd	68.39 f	57.42 de	26.73 bcd	11.90 ab
F66-698	49.62 a	62.44 cdef	73.00 abcd	41.07 g	12.09 ab
D67-6117	48.96 a	58.33 bcdef	57.46 cde	30.96 def	12.99 ab
D69-0263	48.62 a	62.22 cdef	69.25 abcd	33.29 ef	13.11 a
F67-3673	48.48 a	67.99 ef	78.85 abc	32.85 ef	12.03 ab
Tracy	45.66 abcd	60.66 bcdef	65.06 bcde	25.29 abcd	10.47 ab
D68-4641	45.65 abcd	35.11 a	58.24 cde	19.29 a	11.05 ab
Hutton	45.08 abcd	66.88 ef	78.77 abc	32.40 def	12.89 ab
Pickett 71	44.00 cd	60.22 bcdef	53.52 de	29.63 cdef	10.20 ab
Bragg	43.89 d	63.77 def	75.62 abcd	29.29 cdef	13.07 ab
Ransom	43.07 d	66.44 ef	59.31 cde	27.40 bcde	13.30 a

(Continued)

Table 9. Continued

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[1]Mean maturity days after September 1.
[2]Plant height and height of lower pod means in cm.
[3]Mean flowering days after July 1.
[4]Means within a column followed by a letter in common are not significantly different at the 5% probability level according to Duncan's New Multiple Range Test.

protein content among those having different female parents. Four F_2 lines having D69-0263(a) as a female parent, two of F67-3673(a), four of D67-6117(a), four of D68-4641(a), and three of F66-698(a) were all significantly higher in mean protein content than one line of Pickett 71(cd), two of Tracy(bcd,cd), one of Hutton(cd) and three of Bragg(bcd, cd). Also one F_2 line of D69-0263(ab), one of F67-3673(ab), one of D67-6117(ab), and one of D68-4641(ab), were also significantly higher in mean protein than one of Pickett 71(cd), one of Tracy(cd), one of Hutton(cd), and one of Bragg(cd). There were no other significant differences among F_2 lines for mean protein content. The overall coefficient of variation for mean protein content of the parents and F_2 progeny was 4.22%.

Maturity Date Means

Although there were no significant differences among F_2 progeny having the same female parent for mean maturity date, there were significant differences among those having different female parents. Three F_2 lines of D68-4641(a) were significantly earlier maturing than five of D69-0263(cdef,def,ef), six of F67-3673(ef), seven of D67-6117(bcdef, cdef,def,ef), five of F66-698(bcdef,cdef,def,f), two of Pickett 71(cdef, ef), four of Tracy(bcdef,cdef), one of Hutton(ef), and three of Bragg (bcdef,ef,f) (Table 9). The F_2 progeny of D68-4641 x D69-0263 was the next significantly earlier maturing F_2 line and was significant to all of the above mentioned F_2 progeny except the three of D68-4641(a), four of D67-6117(bcdef), two of F66-698(bcdef), one of Tracy(bcdef), and one of Bragg(bcdef). The next significant earlier maturing F_2 progeny were two of D68-4641(abc). These were significantly earlier

maturing than three of D69-0263(def,ef), six of F67-3673(ef), two of D67-6117(def,ef), two of F66-698(def,f), one of Pickett 71(ef), one of Hutton(ef), and two of Bragg(ef,f). Two F_2 progeny of D68-4641(abcd) were significantly earlier maturing than two of D69-0263(ef), six of F67-3673(ef), one of D67-6117(ef), one of F66-698(f), one of Pickett 71 (ef), one of Hutton(ef), and two of Bragg(ef,f). There were no other significant differences among F_2 progeny that have different female parents. The overall coefficient of variation for mean maturity date of the parents and F_2 was 11.72%. In Table 10, it can be seen that 12 or 26% of the maturity date means of the F_2 progeny tended to be like the later maturing parent in exceeding the midparent maturity date means by one or more days. Four or 9% of the F_2 progeny means were later in maturity than their respective later maturing parent. Twenty-two or 49% of the maturity date means of the F_2 progeny tended to be like the earlier maturing parent by being earlier than the midparent maturity date means by one or more days. Seven or 16% of the F_2 progeny means were earlier in maturity than their respective earlier maturing parent mean. Eleven or 24% of the F_2 progeny maturity date means were like the midparent means for maturity date.

It appears that transgressive segregation occurred in several cases where 25% of the F_2 progeny had either later maturity date means than their respective latest maturing parent or earlier maturity date means than their respective earlier maturing parent. The coefficient of variation for mean maturity date of the F_2 progeny was 11.01%.

Table 10. Mean maturity date (after September 1) of parental lines, the midparent, and F_2 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_2	Difference between F_2 and midparent
D69-0263	F66-698	62.22	62.44	62.33	53.94[bc]	-8.39
D69-0263	D67-6117	62.22	58.33	60.28	56.42[cd]	-3.86
D69-0263	Tracy	62.22	60.66	61.44	65.88[be]	4.44
D69-0263	F67-3673	62.22	67.99	65.11	55.47[bc]	-9.64
D69-0263	Hutton	62.22	68.88	65.55	62.40[b]	-3.15
D69-0263	Bragg	62.22	63.77	63.00	63.11[d]	.11
D69-0263	Pickett 71	62.22	60.22	61.22	61.78[b]	.56
D69-0263	Ransom	62.22	66.44	64.33	64.52[d]	.19
F67-3673	F66-698	67.99	62.44	65.22	63.97[d]	-1.25
F67-3673	Tracy	67.99	60.66	64.33	65.89[b]	1.56
F67-3673	Hutton	67.99	68.88	68.44	64.24[bc]	-4.20
F67-3673	Ransom	67.99	66.44	67.22	67.53[b]	.31
F67-3673	Bragg	67.99	63.77	65.88	65.83[d]	- .05
F67-3673	Pickett 71	67.99	60.22	64.11	65.16[b]	1.05
D67-6117	F66-698	58.33	62.44	60.39	61.78[d]	1.39
D67-6117	F67-3673	58.33	67.99	63.16	62.81[b]	- .35
D67-6117	Tracy	58.33	60.66	59.50	56.63[b]	-2.87
D67-6117	Hutton	58.33	66.88	62.61	66.50[d]	3.89
D67-6117	Bragg	58.33	63.77	61.05	60.21[b]	- .84
D67-6117	Pickett 71	58.33	60.22	59.28	58.77[b]	- .51
D67-6117	Ransom	58.33	66.44	62.39	58.34[b]	-4.05
D68-4641	F66-698	35.11	62.44	48.78	52.43[d]	3.65
D68-4641	F67-3673	35.11	67.99	51.55	52.69[d]	1.14
D68-4641	D67-6117	35.11	58.33	46.71	40.62[b]	-6.09
D68-4641	D69-0263	35.11	62.22	48.67	47.61[b]	-1.06
D68-4641	Hutton	35.11	68.88	52.00	55.98[d]	3.98
D68-4641	Pickett 71	35.11	60.22	47.66	50.11[d]	2.45
D68-4641	Bragg	35.11	63.77	49.44	44.86[b]	-4.58
D68-4641	Tracy	35.11	60.66	47.89	43.78[b]	-4.11
D68-4641	Ransom	35.11	66.44	50.78	49.57[b]	-1.21
F66-698	Ransom	62.44	66.44	64.44	60.78[bc]	-3.69
F66-698	Hutton	62.44	68.88	64.66	59.41[bc]	-5.25
F66-698	Tracy	62.44	60.66	65.55	60.10[b]	-1.45
F66-698	Pickett 71	62.44	60.22	61.33	63.71[be]	2.38
F66-698	Bragg	62.44	63.77	63.11	68.40[de]	5.29
Pickett 71	Hutton	60.22	68.88	63.55	64.32[d]	.77
Pickett 71	Ransom	60.22	66.44	63.33	60.95[b]	-2.38

(Continued)

Table 10. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_2	Difference between F_2 and midparent
Tracy	Pickett 71	60.66	60.22	60.44	60.82[b]	.38
Tracy	Hutton	60.66	68.88	63.77	60.70[b]	-3.07
Tracy	Bragg	60.66	63.77	62.22	61.05[b]	-1.17
Tracy	Ransom	60.66	66.44	63.55	58.31[bc]	-5.24
Hutton	Ransom	68.88	66.44	66.66	66.66	0.00
Bragg	Hutton	63.77	68.88	65.33	64.20[b]	-1.13
Bragg	Pickett 71	63 77	60.22	62.00	60.24[d]	-1.76
Bragg	Ransom	63.77	66.44	65.11	68.39[de]	3.28

[a]Coefficient of variation of all maturity date means 11.72%.
[b]F_2 more like female parent in maturity date.
[c]Earlier maturing than its earliest maturing parent.
[d]F_2 more like male parent in maturity date.
[e]Later maturing than its latest maturing parent.

Plant Height Means

There were significant differences among the F_2 progeny of D69-0263 for plant height means. The F_2 progeny of D69-0263 x F67-3673 was significantly taller than the F_2 progeny of D69-0263 x F66-698, D69-0263 x Bragg, D69-0263 x Pickett 71 and D69-0263 x Ransom (Table 9). No other significant differences occurred for plant height means among the other F_2 progeny having the same female parent. There were, as with the other characters discussed, significant differences for plant height means among the F_2 progeny having different female parents. The plant height mean of the F_2 progeny of F67-3673 x Bragg was significantly taller than that of four F_2 progeny means of D69-0263(cde), four of D67-6117(bcde,de), six of D68-4641(bcde,cde,de), one of F66-698(cde), two of Pickett 71(c), three of Tracy(bcde,de), one of Hutton(cde), and two of Bragg(cde,de). The F_2 progeny means of D69-0263 x F67-3673(ab) and F66-3673 x F66-698(ab) were significantly taller than the same F_2 progeny that F67-3673 x Bragg(a) were, except they were not significantly different in plant height means to two F_2 progeny means of D67-6117(bcde), one of D68-4641(bcde) and two of Tracy(bcde). Two F_2 progeny means of F67-3673(abc) had significantly higher plant height means than did two of D67-6117(d), one of D68-4641(de), two of Pickett 71(e), one of Tracy(de), and one of Bragg(de). Two F_2 progeny means of D69-0263(abcd), two of F67-3673(abcd), two of F67-3673(abcd), three of D67-6117(abcd), two of D68-4641(abcd), four of F66-698(abcd), one of Tracy(abcd) and one of Bragg(abcd) had significantly taller plant height means than did the two F_2 progeny of Pickett 71(e). The other F_2 progeny means having different female parents were not different. The

overall coefficient of variation for mean plant height of the parents and F_2 progeny was 16.47%.

Seventeen or 38% of the F_2 progeny means were shorter than their respective midparent plant height means by at least two cm (Table 11). Ten or 22% of the F_2 plant height means tended to be shorter than their respective shortest parent plant height means. Fourteen or 31% of the F_2 progeny means tended to be taller than their respective midparent plant height means by at least two cm. Seven or 16% of the F_2 plant height means tended to be taller than their respective tallest parent plant height means. Fourteen or 31% of the F_2 progeny means tended to be more like their respective midparent means. The data indicates that transgressive segregation occurred in 17 crosses where 36% of the F_2 progeny means were either taller or shorter than their respective tallest or shortest parent. The coefficient of variation for the mean plant height of the F_2 progeny was 16.80%.

Flowering Date Means

There were significant differences for flowering date means among F_2 progeny having the same female parent (Table 9). Significant differences occurred among the F_2 progeny of D69-0263, F67-3673, and D67-6117. There were also significant differences among the F_2 progeny having different female parents. The overall coefficient of variation for mean flowering date of the parents and F_2 progeny was 15.60%.

Twenty-one or 47% of the F_2 progeny tended to have earlier flowering date means, by at least one day, than their respective midparent flowering date means (Table 12). Eleven or 24% of the F_2 progeny had earlier flowering date means than did their respective earliest flowering

Table 11. Mean plant height (in cm) of parental lines, the midparent, and F_2 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_2	Difference between F_2 and midparent
D69-0263	F66-698	69.25	73.00	71.13	62.20[bc]	-8.93
D69-0263	D67-6117	69.25	57.46	63.36	67.10[b]	3.74
D69-0263	Tracy	69.25	65.06	67.16	73.12[bd]	5.96
D69-0263	F67-3673	69.25	78.85	74.05	79.70[de]	5.65
D69-0263	Hutton	69.25	78.77	74.01	69.87[b]	-4.14
D69-0263	Bragg	69.25	75.62	72.44	62.41[bc]	-10.03
D69-0263	Pickett 71	69.25	53.52	61.39	62.41[b]	1.02
D69-0263	Ransom	69.25	59.31	64.28	60.42[e]	-3.86
F67-3673	F66-698	78.85	73.00	75.93	81.63[bd]	5.70
F67-3673	Tracy	78.85	65.06	71.96	77.74[b]	5.78
F67-3673	Hutton	78.85	78.77	78.81	76.11[ce]	-2.70
F67-3673	Ransom	78.85	59.31	69.08	69.41[b]	.33
F67-3673	Bragg	78.85	75.62	77.24	82.77[bd]	5.53
F67-3673	Pickett 71	78.85	53.52	66.19	69.06[b]	2.87
D67-6117	F66-698	57.46	73.00	65.23	67.96[e]	2.73
D67-6117	F67-3673	57.46	78.85	68.16	73.67[e]	5.51
D67-6117	Tracy	57.46	65.06	61.26	67.96[de]	6.70
D67-6117	Hutton	57.46	78.77	68.12	66.97[b]	-1.15
D67-6117	Bragg	57.46	75.62	66.54	65.10[b]	-1.44
D67-6117	Pickett 71	57.46	53.52	55.49	56.14[b]	.65
D67-6117	Ransom	57.46	59.31	58.39	56.63[bc]	-1.76
D68-4641	F66-698	58.24	73.00	65.62	67.33[e]	1.71
D68-4641	F67-3673	58.24	78.85	68.55	65.56[b]	-2.69
D68-4641	D67-6117	58.24	57.46	57.85	54.65[cd]	-3.20
D68-4641	D69-0263	58.24	69.25	63.75	62.67[b]	-1.08
D68-4641	Hutton	58.24	78.77	68.51	67.37[b]	-1.14
D68-4641	Pickett 71	58.24	53.52	55.88	59.17[b]	3.29
D68-4641	Bragg	58.24	75.62	66.93	58.94[b]	-7.99
D68-4641	Tracy	58.24	65.06	61.65	60.90[b]	- .75
D68-4641	Ransom	58.24	59.31	58.78	58.34[b]	- .44
F66-698	Ransom	73.00	59.31	66.16	69.54[b]	3.38
F66-698	Hutton	73.00	78.77	75.89	74.59[b]	-1.30
F66-698	Tracy	73.00	65.06	69.03	72.73[b]	3.70
F66-698	Pickett 71	73.00	53.52	63.26	64.91[b]	1.65
F66-698	Bragg	73.00	75.62	74.31	74.73[e]	.42
Pickett71	Hutton	53.52	78.77	66.15	51.04[bc]	-15.11
Pickett 71	Ransom	53.52	59.31	56.42	48.57[bc]	-7.85

(Continued)

Table 11. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_2	Difference between F_2 and midparent
Tracy	Pickett 71	65.06	53.52	59.29	66.20[bd]	6.91
Tracy	Hutton	65.06	78.77	71.92	67.11[b]	-4.81
Tracy	Bragg	65.06	75.62	70.34	65.68[b]	-4.66
Tracy	Ransom	65.06	59.31	62.19	56.09[ce]	-6.10
Hutton	Ransom	78.77	59.31	69.04	63.64[e]	-5.40
Bragg	Hutton	75.62	78.77	77.20	74.54[bc]	-2.66
Bragg	Pickett 71	75.62	53.52	64.57	61.08[e]	-3.49
Bragg	Ransom	75.62	59.31	67.47	57.42[ce]	-10.05

[a]Coefficient of variation of all plant height means 16.47%.
[b]F_2 more like female parent in plant height.
[c]Shorter than shortest parent.
[d]Taller than tallest parent.
[e]F_2 more like male parent in plant height.

Table 12. Mean flowering date (after July 1) of parental lines, the midparent, and F_2 population grown on Olivier silt loam, Baton Rouge, 1973.[a]

Cross combination Female	Male	P_1	P_2	Midparent	F_2	Difference between F_2 and midparent
D69-0263	F66-698	33.29	41.07	37.18	26.55[bc]	-10.63
D69-0263	D67-6117	33.29	30.96	32.13	38.02[bd]	5.89
D69-0263	Tracy	33.29	25.29	29.29	32.41[b]	3.12
D69-0263	F67-3673	33.29	32.85	33.07	32.26[ce]	- .81
D69-0263	Hutton	33.29	32.40	32.85	30.37[ce]	-2.48
D69-0263	Bragg	33.29	29.29	31.29	31.22[e]	- .07
D69-0263	Pickett 71	33.29	29.63	31.46	31.34[e]	- .12
D69-0263	Ransom	33.29	27.40	30.35	29.65[e]	- .70
F67-3673	F66-698	32.85	41.07	36.96	38.50[e]	1.54
F67-3673	Tracy	32.85	25.29	29.07	28.99[e]	- .08
F67-3673	Hutton	32.85	32.40	32.63	32.60[e]	- .03
F67-3673	Ransom	32.85	27.40	30.13	30.69[b]	.59
F67-3673	Bragg	32.85	29.29	31.07	30.71[e]	- .36
F67-3673	Pickett 71	32.85	29.63	31.24	31.40[b]	.16
F67-6117	F66-698	30.96	41.07	36.02	35.19[b]	- .83
D67-6117	F67-3673	30.96	32.85	31.91	30.90[bc]	-1.01
D67-6117	Tracy	30.96	25.29	28.13	25.62[e]	-2.51
D67-6117	Hutton	30.96	32.40	31.68	30.95[bc]	- .73
D67-6117	Bragg	30.96	29.29	30.13	30.60[e]	.47
D67-6117	Pickett 71	30.96	29.63	30.30	28.21[ce]	-2.09
D67-6117	Ransom	30.96	27.40	29.18	27.65[e]	-1.53
D68-4641	F66-698	19.29	41.07	30.18	25.03[b]	-5.15
D68-4641	F67-3673	19.29	32.85	26.07	22.04[b]	-4.03
D68-4641	D67-6117	19.29	30.96	25.13	20.80[b]	-4.33
D68-4641	D69-0263	19.29	33.29	26.29	26.86[e]	.60
D68-4641	Hutton	19.29	32.40	25.85	23.06[e]	2.79
D68-4641	Pickett	19.29	29.63	24.46	20.56[b]	-3.90
D68-4641	Bragg	19.29	29.29	24.29	20.34[b]	-3.94
D68-4641	Tracy	19.29	25.29	22.29	19.71[b]	-2.58
D68-4641	Ransom	19.29	27.40	23.35	20.92[b]	-2.43
F66-698	Ransom	41.07	27.40	34.24	35.19[b] [e]	.95
F66-698	Hutton	41.07	32.40	36.74	34.03[e]	-2.71
F66-698	Tracy	41.07	25.29	33.18	29.92[b]	-3.26
F66-698	Pickett 71	41.07	29.63	35.35	32.35[e]	-3.00
F66-698	Bragg	41.07	29.29	35.18	34.24[e]	- .94
Pickett 71	Hutton	29.63	32.40	31.02	29.07[bc]	-1.95
Pickett 71	Ransom	29.63	27.40	28.52	25.27[ce]	-3.20

(Continued)

Table 12. Continued

Cross combination Female	Male	P_1	P_2	Midparent	F_2	Difference between F_2 and midparent
Tracy	Pickett 71	25.29	29.63	27.46	26.22[b]	-1.24
Tracy	Hutton	25.29	32.40	28.85	23.99[bc]	4.89
Tracy	Bragg	25.29	29.29	27.29	29.72[de]	2.43
Tracy	Ransom	25.29	27.40	26.35	25.37[b]	- .98
Hutton	Ransom	32.40	27.40	29.90	28.94[e]	- .96
Bragg	Hutton	29.29	32.40	30.85	31.57[e]	.92
Bragg	Pickett 71	29.29	29.63	29.46	27.92[bc]	-1.54
Bragg	Ransom	29.29	27.40	28.35	26.73[ce]	-1.62

[a]Coefficient of variation of all flowering date means 15.60%.
[b]F_2 more like female parent in flowering date.
[c]Earlier flowering than earliest flowering parent.
[d]Later flowering than latest flowering parent.
[e]F_2 more like male parent in flowering date.

parent. Five or 11% of the F_2 progeny had later flowering date means, by at least one day, than their respective midparent. Two or 4% of the F_2 progeny had later flowering dates than did their respective later flowering parent. Nineteen or 42% of the F_2 progeny had flowering date means similar to their midparent. It can be seen from this that there was a tendency for the F_2 progeny of these crosses to either have earlier flowering dates or to be intermediate between both parents for flowering dates. The coefficient of variation for the mean flowering date of the F_2 progeny was 14.63%.

There were no significant differences for height of lower pod means among F_2 progeny having the same female parent (Table 9). The only significant difference among F_2 progeny not having the same female parent was D69-0263 x Tracy, which had a significantly higher lower pod mean than did the F_2 progeny of Pickett 71 x Ransom. The overall coefficient of variation for height of lower pod means of the parents and F_2 progeny was high at 39.73%.

Heritability

Broad sense heritabilities of the various cross combinations for protein, maturity date, plant height, flowering date, and height of lower pods are shown in Table 13. Most of the heritabilities for protein were moderate to high, but ranged from .09 to .90. The high protein lines D67-6117, F66-698, and F67-3673 used as the female parent had high general combining ability. Heritabilities as an average of seven crosses for D67-6117, six for F67-3673, and five for F66-698 were .81, .78, and .79, respectively. D67-6117 x F66-698 and F66-698 x Hutton had heritabilities of .90. High heritabilities were not limited to high

Table 13. Heritability estimates for protein, maturity date, plant height, flowering date and height of lower pod for the F_2 population grown on Olivier silt loam, Baton Rouge, 1973.

Cross combination Female	Male	Protein	Maturity date	Plant height	Flowering date	Height of lower pod
D69-0263 x	F66-698	.71 [1/]	.54	.57	.81	.58
		(4.22) [1/]	(17.36)	(18.91)	(21.73)	(34.53)
D69-0263 x	D67-6117	[2/]	- .24	.79	.84	.65
		(1.95)	(10.29)	(21.66)	(13.73)	(35.00)
D69-0263 x	Tracy	.32	[2/]	.54	.75	.87
		(3.18)	(5.09)	(16.95)	(12.01)	(37.08)
D69-0263 x	F67-3673	.19	.90	.27	.62	.78
		(4.19)	(23.84)	(13.49)	(12.29)	(34.26)
D69-0263 x	Hutton	.63	.61	.51	.53	.70
		(4.40)	(12.61)	(15.82)	(11.50)	(37.85)
D69-0263 x	Bragg	.64	[2/]	.57	.65	.33
		(4.52)	(6.34)	(16.96)	(12.71)	(37.34)
D69-0263 x	Pickett 71	.60	[2/]	.60	.65	.88
		(4.79)	(5.60)	(17.22)	(11.20)	(44.56)
D69-0263 x	Ransom	.59	.29	.35	.88	.58
		(5.05)	(5.50)	(16.66)	(18.37)	(32.98)
F67-3673 x	F66-698	.85	.87	.44	.44	.23
		(4.68)	(9.75)	(11.92)	(7.47)	(35.35)
F67-3673 x	Tracy	.74	-.10	.45	.80	.58
		(4.09)	(3.98)	(13.31)	(12.80)	(42.05)
F67-3673 x	Hutton	.80	.97	.51	.77	.70
		(4.62)	(16.72)	(13.50)	(13.00)	(42.16)
F67-3673 x	Ransom	.77	[2/]	.65	.91	.35
		(5.02)	(2.14)	(18.18)	(17.25)	(44.37)
F67-3673 x	Bragg	.75	.34	.67	.70	.57
		(4.19)	(4.88)	(13.36)	(11.91)	(36.98)
F67-3673 x	Pickett 71	.81	.61	.72	.74	.63
		(5.28)	(4.43)	(17.21)	(11.47)	(37.08)
D67-6117 x	F66-698	.90	.09	.66	.80	.05
		(4.47)	(5.79)	(12.93)	(11.72)	(32.22)

(Continued)

Table 13. Continued

Cross combination Female	Male	Protein	Maturity date	Plant height	Flowering date	Height of lower pod
D67-6117	F67-3673	.57	.74	.68	.83	.68
		(3.41)	(7.09)	(14.90)	(13.78)	(37.07)
D67-6117	Tracy	.84	.43	.58	.85	.35
		(4.07)	(9.52)	(12.36)	(14.18)	(30.55)
D67-6117	Hutton	.87	2/	.40	.68	.39
		(4.56)	(2.38)	(10.07)	(9.57)	(28.90)
D67-6117	Bragg	.82	-.14	.75	.76	.25
		(3.90)	(6.16)	(14.23)	(11.42)	(30.70)
D67-6117	Pickett 71	.84	-.26	.86	.83	.57
		(4.59)	(4.18)	(21.85)	(12.91)	(36.78)
D67-6117	Ransom	.83	.82	.44	.89	.39
		(4.70)	(13.25)	(12.80)	(14.72)	(27.56)
D68-4641	F66-698	.83	.79	.77	.77	.24
		(4.35)	(17.18)	(19.72)	(19.41)	(34.42)
D68-4641	F67-3673	.40	.92	.62	.77	.47
		(3.75)	(27.06)	(18.72)	(21.03)	(35.88)
D68-4641	D67-6117	.64	.85	.78	.75	-.02
		(3.90)	(26.19)	(21.36)	(18.17)	(29.87)
D68-4641	D69-0263	.41	.43	.51	.69	.70
		(5.01)	(21.46)	(18.74)	(21.41)	(34.21)
D68-4641	Hutton	.65	.83	.77	.76	.39
		(3.54)	(13.54)	(19.55)	(19.21)	(29.46)
D68-4641	Pickett 71	.63	.33	.88	.78	.59
		(3.88)	(16.93)	(27.55)	(19.55)	(39.89)
D68-4641	Bragg	.72	.78	.64	.78	-.04
		(4.02)	(22.39)	(16.01)	(22.52)	(32.28)
D68-4641	Tracy	.54	.74	.36	.82	.35
		(3.27)	(22.03)	(14.02)	(21.30)	(31.30)
D68-4641	Ransom	.09	.76	.50	.77	.39
		(3.55)	(16.03)	(16.05)	(17.04)	(33.06)

(Continued)

Table 13. Continued

Cross combination Female	Male	Protein	Maturity date	Plant height	Flowering date	Height of lower pod
F66-698	Ransom	.64 (2.43)	-.47 (4.40)	.37 (11.33)	.51 (5.96)	.44 (35.72)
F66-698	Hutton	.90 (3.92)	-.34 (3.76)	.34 (9.91)	.83 (15.12)	.31 (35.00)
F66-698	Tracy	.70 (2.36)	.64 (11.23)	.66 (15.21)	.76 (11.61)	.46 (39.23)
F66-698	Pickett 71	.84 (3.62)	.03 (4.34)	.77 (16.99)	.82 (13.24)	.31 (33.52)
F66-698	Bragg	.87 (3.62)	.71 (10.56)	.65 (12.16)	.74 (12.00)	.38 (39.57)
Pickett 71	Hutton	.86 (4.52)	.78 (6.91)	.69 (18.74)	.90 (18.89)	.70 (38.41)
Pickett 71	Ransom	.71 (3.76)	.91 (14.21)	.66 (19.55)	.82 (12.39)	.19 (30.54)
Tracy	Pickett 71	.73 (3.32)	.46 (7.28)	.86 (22.73)	.77 (11.30)	.69 (38.16)
Tracy	Hutton	.83 (3.70)	.78 (10.74)	.89 (29.20)	.86 (18.35)	.68 (40.19)
Tracy	Bragg	.81 (3.58)	.67 (13.35)	.83 (21.34)	.90 (16.79)	.55 (34.97)
Tracy	Ransom	.73 (3.53)	.21 (7.49)	.57 (19.03)	.87 (15.80)	.60 (35.64)
Hutton	Ransom	.82 (4.30)	.74 (7.28)	.66 (16.93)	.83 (13.60)	.54 (33.49)
Bragg	Hutton	.79 (3.31)	.55 (6.96)	.82 (17.12)	.84 (15.37)	.32 (28.91)
Bragg	Pickett 71	.87 (4.84)	.75 (10.39)	.73 (14.90)	.18 (6.76)	-.34 (26.69)
Bragg	Ransom	.77 (3.76)	2/ (.91)	.55 (14.66)	.86 (15.67)	.60 (35.00)

Table 13. Continued

Cross combination						
Female	Male	Protein	Maturity date	Plant height	Flowering date	Height of lower pod
	$h_{\bar{x}}$	.70	.50	.63	.76	.46
	$CV_{\bar{x}}$	4.00	11.72	16.80	14.63	35.13

1/Coefficient of variation.

2/Heritability estimates were left out of the table because they were not realistic.

protein x high protein lines as high heritabilities were also obtained with other combinations including low protein x low protein lines. Heritability as an average of all lines was .70 and the coefficient of variation was 4.0%. This shows that selection for protein on an individual plant basis would be effective. This has been found by others (9, 43, 74).

Heritability of maturity date was variable among the various cross combinations, but was generally moderately high to high. Some of the plants did not mature normally making the date of maturity difficult to determine. Consequently some of the parents were more variable in maturity date than the F_2. As an average of all crosses, heritability for maturity date was .50. This was lower than expected and lower than that reported in the literature (9, 43).

Plant height generally had moderate to high heritabilities, ranging from .27 to .89. This indicated that good progress could be made selecting for plant height in the F_2 generation. Mean heritability for plant height of all F_2 progeny tested was .63 and the mean coefficient of variation was 16.8%. Heritabilities similar to this mean heritability has been reported by other researchers (9, 43, 46, 78).

Heritabilities for flowering date for the F_2 progenies were also quite variable ranging from .18 to .91. However, 21 cross combinations had heritabilities of .80 or higher for flowering date with the average of all combinations .76. This was similar to that found by others (9, 43, 46).

Heritabilities for height of lower pods were generally moderately low among the various F_2 progenies and were quite variable. The average of all the cross combinations tested was .46 and the coefficient of

variation was 35.13%. This was the lowest heritability for the characters studied, but indicated that some progress could be made selecting for lower pod height in the F_2 generation. This was a little lower than the heritability estimates reported by Martin and Wilcox (57).

This experiment was conducted at only one location and in one year. Therefore, the data are biased with years and location effects that could not be removed. The heritability estimates may be somewhat overestimated, but are generally in agreement with those reported in the literature.

Variability of Parents

Table 14 shows the means, variances, and coefficients of variation for each selected character studied for the 10 parental lines grown with the F_2 population. It can be seen from this table that one parental line (D69-0263) may have been heterogeneous. The variances and coefficients of variation for D69-0263 were higher in all selected characters, except one, than they were for the other parental lines. The variances and coefficients of variation for D68-4641 were also fairly high for most characters which may indicate that it too may not have been homogeneous.

Protein Frequency Distributions

Tables 15-20 show the frequency distributions of the parents and F_2 plants for protein content. The means, midparent, standard deviation, and number of plants within each frequency distribution are included in each table. Protein percentage classes range from 38 to 53 with each class representing a range of 0.5% protein. The female

Table 14. Means, variances, and coefficients of variation for selected plant characters of 10 parental lines grown on Olivier silt loam with the F_2 generation, Baton Rouge, 1973.

Plant character and statistic	Plant lines									
	F66-698	D67-6117	D69-0263	F67-3673	Tracy	D68-4641	Hutton	Pickett 71	Bragg	Ransom
Protein										
Mean	49.62	48.96	48.62	48.48	45.66	45.66	45.06	44.00	43.89	43.07
Variance	0.30	0.76	5.51	1.92	0.51	2.06	0.47	0.73	0.47	0.87
C.V.	1.10	1.78	4.83	2.86	1.56	3.14	1.53	1.94	1.57	2.17
Flowering date (after July 1)										
Mean	38.00	30.96	33.29	32.85	25.29	16.67	32.40	29.63	29.29	27.40
Variance	5.0	2.25	8.25	4.36	1.75	5.75	4.03	2.25	3.75	1.53
C.V.	5.75	4.85	8.63	6.36	5.23	14.39	6.19	5.06	6.61	4.51
Maturity date (after Sept. 1)										
Mean	62.44	58.33	62.22	67.99	60.66	34.22	66.88	60.22	63.77	66.44
Variance	11.44	12.00	145.53	2.25	23.25	24.69	3.94	4.78	20.61	9.69
C.V.	5.42	5.94	19.39	2.21	7.95	14.52	2.97	3.63	7.12	4.69
Plant height in cm										
Mean	73.00	57.46	69.25	78.85	65.06	57.22	78.77	53.52	75.62	59.31
Variance	35.16	20.21	99.99	71.93	49.19	45.00	36.62	21.39	23.21	43.39
C.V.	8.12	7.82	14.44	10.76	10.78	11.72	7.68	8.64	6.37	11.11
Height of lower pod in cm										
Mean	12.09	12.99	13.11	12.03	10.48	11.05	12.89	10.20	13.07	13.30
Variance	16.22	9.53	2.28	7.29	4.37	6.97	6.36	3.81	12.39	3.94
C.V.	33.31	23.77	11.51	22.44	19.96	23.90	19.57	19.12	26.93	14.93

parent was listed first in each frequency distribution. The frequency distributions were generally grouped into the same table where the F_2 progeny have the same female parent. The description and explanation of one frequency distribution is impossible as a result of the very small F_2 population obtained for that particular cross combinations. The discussion of the frequency distributions will be by female parent. The expected genetic advance for each frequency distribution will also be included in this part of the discussion (Table 21).

In the frequency distribution tables none of the F_2 progeny fit all the characteristics expected of a normally distributed quantitative character. However, protein content in soybeans is thought to be controlled by many genes thereby making it a quantitative character. The characteristics that are not typical of a normal distribution will be pointed out for each frequency distribution discussed below. Unless otherwise stated, the difference in mean protein percent of the parents were not significant at the 5% level.

D69-0263

The frequency distributions for the F_2's and male lines having D69-0263 as the common female parent are presented in Table 15. Although somewhat repetitious, the range of the female parent will be stated for each cross combination.

D69-0263 x F66-698

The range in protein content for D69-0263 was from 43.94 to 50.57% while the range for F66-698 was from 48.94 to 50.64%. The mean

Table 15. Frequency distributions, means, and standard deviations for protein percent of the D69-0263 x selected male parents and the F_2's grown on Olivier silt loam, Baton Rouge, 1973.

Parents and generations[1/]	Protein percent																									Protein content means[2/]	s	Number of plants
	40	41	42	43	44		45		46		47		48		49		50		51		52	53						
D69-0263					1			1					1		1		2	3								48.62	2.35	9
F66-698															2	4	1	2								49.62	.54	9
F_2								1		1	4		3	5	3	4	6	9	7	3	1					49.78	2.10	47
Midparent																										49.12		
D69-0263					1			1					1		1		2	3								48.62	2.35	9
D67-6117													1	4		2	1	1								48.96	.87	9
F_2															2	1			1							49.63	.97	4
Midparent																										48.79		
D69-0263					1			1					1		1		2	3								48.62	2.35	9
Tracy						2	1		4	2																45.66	.71	9
F_2							2	2	1	1	1	5	2	6	6	5	7	12	3	1						49.12	1.56	54
Midparent																										47.14		
D69-0263					1			1					1		1		2	3								48.62	2.35	9
F67-3673								1					1	2	1	3	1									48.48	1.39	9
F_2					2	1	1	2		1	1	4	2	7	4	2	3	2	2		1					47.74	2.00	35
Midparent																										48.55		
D69-0263					1			1					1		1		2	3								48.62	2.35	9
Hutton					1		5	2		1																45.08	.69	9
F_2		1		1	1	2	3	1	1	2	7	10	3	2	1	1	3					1				47.17	2.08	40
Midparent																										46.85		
D-69-0263					1			1					1		1		2	3								48.62	2.35	9
Bragg				1	2	3	1	2																		43.89	.69	9
F_2			1		3	2	3	1	5	5	5	7	3	1	5	1	2	3	1	2						46.96	2.12	45
Midparent																										46.26		

(Continued)

Table 15. Continued

Parents and generations[1]	Protein percent																									Protein content means[2]	s	Number of plants
	40	41	42		43		44		45		46		47		48		49		50		51		52		53			
D69-0263							1			1					1		1		2	3						48.62	2.35	9
Pickett 71				1	1	1	2	2	1	1																44.00	.86	9
F_2	1			2		2	4	2	6	5	11	5	7	8	7	4	4	2	5		2	2	1			46.92	2.25	80
Midparent																										46.31		
D69-0263							1			1					1		1		2	3						48.62	2.35	9
Ransom			1	2	3	2				1																43.07	.93	9
F_2		3	1	1	6	3	2	4	2	5	3	4	6	2	5	3	4	2								45.80	2.31	56
Midparent																										45.85		

1/Female parent listed first.
2/Protein in percent.

of the two parents was 48.62 and 49.62%, respectively. The midparent was 49.12%.

The range in protein content of the 47 F_2 plants was from 45.30 to 52.46%. There was a moderate number of classes and the F_2's were continuously distributed, which was typical for a quantitative trait. There were some components of this distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 50.50% protein which contained 9 plants or 19% of the progeny. The mean of the F_2 should equal the midparent mean. However, in this case the F_2 mean was 49.78% protein which was .66% more than the midparent mean and significant at .05 probability level according to the t test. There were 17 plants or 36% of the F_2's which fell below the midparent means while 30 plants or 64% of the F_2's were above this value. In this F_2 population the median was 49.25%, and the midrange was 48.88% protein. There were 11 plants or 23% of the F_2's above the range of the high protein parent, F66-698. These are the factors which cause this F_2 progeny to be unlike a normally distributed quantitative character.

None of the F_2 progeny were above or below the range of two standard deviations from the F_2 mean. Anything occurring two standard deviations either above or below the mean would place that particular portion of a frequency distribution where 2.5% of the progeny of a population is expected to occur. Anything falling within these upper and lower critical regions is accepted by researchers as being significant.

The expected advance for this F_2 progeny was 2.64% protein. When this is added to the F_2 mean of 49.78% protein, it gives an expected

mean of 52.42% protein. This expected mean is the mean protein percent that the F_3 generation is expected to have when the highest 10% of the F_2 population is selected for parents for the F_3 generation. This means that the five F_2 plants having the highest protein content in this F_2 population would be selected as parents for the F_3 generation.

D69-0263 x D67-6117

This frequency distribution will not be discussed as there were only 4 F_2 progeny. This is not enough progeny to indicate the performance of the F_2 or to draw any conclusion about them.

D69-0263 x Tracy

Protein content for D69-0263 ranged from 43.94 to 50.57% while the range for Tracy was from 44.61 to 46.27%. The mean of the two parents were 48.62 and 45.66%, respectively. The midparent mean was 47.44%.

The 54 F_2 plants ranged from 45.00 to 51.33% protein. There was a moderate number of classes, and the F_2's were continuously distributed. There were some components of this distribution, which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 was 50.50% protein which contained 12 plants or 22% of the progeny. The F_2 mean was 49.12% protein which was 1.98% more protein than the midparent mean. This difference was highly significant. There were 47 plants or 87% of the F_2's above the midparent mean while 7 plants or 13% of the F_2's were below this value. There was a very noticeable tendency for more of the F_2's to have more protein content than the midparent mean. The F_2 population median was 47.50%, and the midrange was 48.17% protein. There were four plants or

7% of the F_2's which were above the range of the high protein parent, D69-0263.

None of the F_2 progeny were above, but there were four plants below the range of two standard deviations of the F_2 mean.

The expected advance for this F_2 progeny was .88%. When this is added to the F_2 mean of 49.12% protein, it gives an expected F_3 mean of 50.00% protein.

D69-0263 x F67-3673

The range in protein content for D69-0263 was from 43.94 to 50.57% while the range for F67-3673 was from 45.44 to 49.90%. The mean of the two parents was 48.62 and 48.48%, respectively. The midparent mean was 48.55%.

Protein content of the 35 F_2 plants ranged from 43.65 to 51.60%. There was a moderate number of classes and the F_2's were continuously distributed. There were some components of this distribution, which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 48.00% protein which contained 7 plants or 20% of the progeny. The F_2 mean was 47.74% protein which was significantly less than the midparent mean by .81% protein. There were 25 plants or 71% of F_2's which fell below the midparent mean while 10 plants or 29% of the F_2's were above this value. There was a very noticeable tendency for more of the F_2's to have less protein content than the midparent mean. The median was 47.50%, and the midrange was 47.63% protein in this F_2 population. There was one plant or 3% of the F_2's which was above the range of the high protein parent,

D69-0263, and two plants or 6% which were below the range of the lower protein parent, F67-3673.

No F_2 progeny were two standard deviations from the mean. The expected advance for this F_2 progeny was .67% protein. This added to the F_2 mean of 47.74% protein gives an expected mean of 48.41% protein for the F_3 population.

D69-0263 x Hutton

D69-0263 ranged from 43.94 to 50.57% protein while the range for Hutton was from 44.11 to 46.61%. The mean of the two parents was 48.62 and 45.08%, respectively. The midparent mean was 46.85% protein.

The range in protein content of the 40 F_2 plants was from 40.95 to 52.48%. There were a moderate number of classes and the F_2's were continuously distributed. There were some components of the distribution, which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 47.50% protein which contained 10 plants or 25% of the progeny. The F_2 mean was 47.17% which exceeded the midparent mean by .32% protein but was not significantly higher. There were 28 plants or 70% of the F_2's above the midparent mean while 12 plants or 30% of the F_2's were below this value. In this F_2 population the median was 46.50%, and the midrange was 46.72% protein. There was one plant or 3% of the F_2's above the range of the high protein parent, D69-0263, and two plants or 5% which fell below the range of the low protein parent, Hutton.

There was one F_2 plant above, and two F_2 plants below two standard deviations of the F_2 mean.

The expected advance for this F_2 progeny was 2.31% protein which would give an expected mean of 49.48% protein in the F_3 generation.

D69-0263 x Bragg

The range in protein content for D69-0263 was from 43.94 to 50.57% while the range for Bragg was from 42.67 to 44.77%. The difference in the parents for protein content was significant (Table 9). The two parents mean protein content was 48.62 and 43.89%, respectively. The midparent mean was 46.26% protein.

The 45 F_2 plants ranged from 41.91 to 51.13% protein. There were a moderate number of classes, and the F_2's were continuously distributed. There were some components of the distribution, which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 47.00% protein which contained 7 plants or 16% of the progeny. The F_2 mean was 46.96% which was significantly more than the midparent mean by .70% protein. There were 28 plants or 62% of the F_2's which were above the midparent mean while 17 plants or 38% of the F_2's were below the value. There were two plants or 4% of the F_2's which were above the range of the high protein parent, D69-0263, and one plant or 2% which fell below the range of the low protein parent, Bragg.

One F_2 plant was two standard deviations above the F_2 mean.

The expected advance for this F_2 progeny was 2.39% protein. This added to the F_2 mean of 47.17% protein gave an expected F_3 mean of 49.35% protein.

D69-0263 x Pickett 71

The range in protein content for D69-0263 was from 43.94 to 50.57% while the range for Pickett 71 was from 42.52 to 45.27%. The difference in the parents for protein content was significant (Table 9). The mean protein content of the two parents were 48.62 and 44.00%, respectively. The midparent mean was 46.31% protein.

Protein content of the 80 F_2 plants ranged from 40.38 to 52.00%. The F_2's were continuously distributed and there were a large number of classes. The modal class of the F_2 progeny was 46.00% protein which contained 11 plants or 14% of the progeny. The F_2 mean was 46.92% which was more than the midparent mean by .61% protein and the difference was highly significant. There were 47 plants or 59% of the F_2's above the midparent mean while 33 plants or 41% of the F_2's were below that value. The median of this F_2 population was 47.50%, and the midrange was 46.19%. There were five plants or 6% of the F_2's which were above the range of the high protein parent, D69-0263, and one plant or 1% which fell below the range of the low protein parent, Pickett 71.

There was one F_2 plant above and one below two standard deviations of the F_2 mean.

The expected advance for this F_2 progeny was 2.38% protein which would give an expected F_3 mean of 49.35% protein.

D69-0263 x Ransom

D69-0263 ranged in protein content from 43.94 to 50.57% while Ransom ranged from 41.94 to 45.24%. The difference in the parents for protein content was significant (Table 9). The mean protein content of

the two parents was 48.62 and 43.08%, respectively. The midparent mean was 45.85% protein.

Protein content of the 56 F_2 plants ranged from 41.27 to 49.59%. There were a moderate number of classes, and the F_2's were continuously distributed. There were some components of the distribution, which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 43.00% protein which contained six plants or 11% of the progeny. The F_2 mean was 45.80% which was only .05% lower than the midparent which was not significant. There were 29 plants or 52% of the F_2's above the midparent mean while 27 plants or 48% of the F_2's were below that value. There were three of the F_2's which were below the range of the low protein parent, Ransom, and none above the range of the high protein parent, D69-0263.

No F_2 progeny were outside the range of two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.40% protein. This added to the F_2 mean of 45.80% protein gave an expected mean of 48.20% protein.

F67-3673

Frequency distributions for the F_2's and male lines having F67-3673 as the common female parent are shown in Table 16.

F67-3673 x F66-698

The range in protein content for F67-3673 was from 45.44 to 49.90% while the range for F66-698 was from 48.94 to 50.64%. The two parents

Table 16. Frequency distribution, means, and standard deviations for protein percent of F67-3673 x selected male parents and F_2's grown on Olivier silt loam, Baton Rouge, 1973.

Parents and generations[1/]	Protein percent																									Protein content means[2/]	s	Number of plants
	40	41	42	43	44	45	46	47	48	49	50	51	52	53														
F67-3673							1								1	2	1	3	1							48.48	1.39	9
F66-698																2	4	1	2							49.62	.54	9
F_2						1		1	1	2	5	7	5	5	11	7		4	2			2				48.89	2.29	53
Midparent																										49.05		
F67-3673							1								1	2	1	3	1							48.48	1.39	9
Tracy						2	1		4	2																45.66	.71	9
F_2		1			2	3	4	2	2	5	4	6	7	12	6	4	6	5	1	2						47.87	1.96	72
Midparent																										47.07		
F67-3673							1								1	2	1	3	1							48.48	1.39	9
Hutton					1	5	2		1																	45.08	.69	9
F_2		1		1	3	2	4	1	6	3	4	8	5	3	6	6	5	8		1						47.22	2.18	67
Midparent																										46.78		
F67-3673							1								1	2	1	3	1							48.48	1.39	9
Ransom			1	2	3	2	1																			43.07	.93	9
F_2			2	2		1	1	2	3	5	3	2	2	2	3	3	3	4	2	1						46.75	2.35	41
Midparent																										45.78		
F67-3673							1								1	2	1	3	1							48.48	1.39	9
Bragg					1	2	3	1	2																	43.89	.69	9
F_2				1	2	2	4	5	3	9	4	6	9	7	7	2	3	1		2	1	1				46.58	1.95	69
Midparent																										46.19		
F67-3673							1								1	2	1	3	1							48.48	1.39	9
Pickett 71				1	1	1	2	2	1	1																44.00	.86	9
F_2		3	2	2		1	8	2	7	10	9	5	9	5	7	3	5	5	3	1	6	1				46.68	2.47	94
Midparent																										46.24		

1/Female parent listed first.
2/Protein in percent.

had a mean protein content of 48.48 and 49.62%, respectively. The midparent mean was 49.05% protein.

The 53 F_2 plants ranged from 44.55 to 52.42% in protein. There was a moderate number of classes, and the F_2's were continuously distributed. There were some components of the distribution, which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 49.00% protein which contained 11 plants or 21% of the progeny. The F_2 mean was 48.89% which was not significantly below the midparent mean. There were 15 plants or 28% of the F_2's which had more protein than the midparent mean while 38 plants or 72% of the F_2's were below that value. There were 8 plants or 15% of the F_2's above the range of the high protein parent, F66-698, and one plant or 2% which fell below the range of F67-3673, the lower protein parent.

No F_2 progeny occurred outside the range of two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.43% protein. The F_2 mean of 48.89% protein plus the expected advance would give an expected mean of 52.32% protein in the F_3 generation.

F67-3673 x Tracy

Protein content for F67-3673 ranged from 45.44 to 49.90% while Tracy ranged from 44.61 to 46.61%. The mean protein content of the two parents were 48.48 and 45.66%, respectively. The midparent mean was 47.07% protein.

Protein content ranged from 41.24 to 51.50% for the F_2 plants. There was a moderately large number of classes, and the F_2 were

continuously distributed. There were some components of the distribution, which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 48.50% which contained 12 plants or 17% of the progeny. The F_2 mean was 47.87% which exceeded the midparent mean by .80% protein and was highly significant. There were 49 plants or 68% of the F_2's which exceeded the midparent mean and 23 plants or 32% of the F_2's below that value.

The median of this F_2 population was 47.50% and the midrange was 46.37%. There were 8 plants or 11% of the F_2's which occurred above the range of the high protein parent, F67-3673, and 3 plants or 4% below the range of Tracy, the low protein parent.

There was one F_2 plant which fell below and none above two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.55% protein. This figure added to the F_2 mean of 47.87% protein gave an expected F_3 mean of 50.42% protein.

F63-3673 x Hutton

The range in protein content for F63-3673 was from 45.44 to 49.90% while Hutton ranged from 44.11 to 46.61%. The mean protein content of the two parents was 48.48 and 45.08%, respectively. The midparent mean was 46.78% protein.

The 67 F_2 plants ranged in protein content from 40.99 to 51.55%. There was a moderately large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed

quantitative character. There were two modal classes of the F_2 progeny, 47.00 and 50.00%, and each contained 8 plants or 12% of the progeny. The F_2 mean was 47.22% which was .44% more protein than the midparent mean but it was not significantly different. There were 42 plants or 63% of the F_2's above the midparent mean while 25 plants or 37% of the F_2's were below that value. This F_2 population had a median of 46.50%, and a midrange of 46.27%. There was one plant or 2% of the F_2's above the range of F67-3673, the high protein parent, and five plants or 8% below the range of the low protein parent, Hutton.

There was one F_2 plant below and none above two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.07% protein. The F_2 mean of 47.22% protein plus the 3.07% gave an expected F_3 mean of 50.29% protein.

F67-3673 x Ransom

F67-3673 ranged in protein content from 45.44 to 49.90% while the range for Ransom was from 41.94 to 45.24%. The difference in parents for protein content was significant (Table 9). The mean protein content of the two parents was 48.48 and 43.07%, respectively. The midparent mean was 45.78% protein.

The 41 F_2 plants ranged in protein content from 41.92 to 50.25%. There was a moderate number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 45.50% which contained 5 plants or 12% of the progeny. The F_2 mean was 46.75% which

was .97% more than the midparent mean and highly significant to it. There were 25 plants or 61% of the F_2's which exceeded the midparent mean while 16 plants or 39% of the F_2's were below that value. The median of this F_2 population was 46.50% and the midrange was 46.09%. There was one plant or 2% of the F_2's above the range of F67-3673, the high protein parent, and there were not any which fell below the range of the low protein parent, Ransom.

No F_2 plants were above, but there was one plant that fell below two standard deviations of the F_2 mean.

The F_2 progeny had an expected genetic advance of 3.18% protein. This figure added to the F_2 mean of 46.75% protein gave an expected mean for the next generation of 49.93% protein.

F67-3673 x Bragg

The range in protein content for F63-3673 was from 45.44 to 49.90% while Bragg ranged from 42.67 to 44.77%. The difference in parents for protein content was significant (Table 9). The mean protein content of the two parents was 48.48 and 43.89%, respectively. The midparent mean was 46.19% protein.

Protein content of the 69 F_2 plants ranged from 42.58 to 51.37%. The F_2 were continuously distributed and there was a moderately large number of classes. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. There were two modal classes of the F_2 progeny. These were 45.50 and 47.00% protein and each contained 9 plants or 13% of the progeny. The F_2 mean was 46.58% which surpassed the midparent mean by .39% protein but was not significant. Thirty-nine plants or 57%

of the F_2's exceeded the midparent mean while 30 or 43% of the F_2's were less than that value. This F_2 population had a median of 46.75% and a midrange of 46.88%. There were 4 plants or 6% of the F_2's which surpassed the range of the high protein parent, F67-3673, and one plant or 2% which fell below the range of Bragg, the low protein parent.

There were two F_2 plants above and one below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.57% protein. This figure added to the F_2 mean of 46.58% protein gave an expected F_3 mean of 49.15% protein.

F67-3673 x Pickett 71

F67-3673 ranged in protein content from 45.44 to 49.90% while the range for Pickett 71 was from 42.52 to 45.27%. The difference in parents for protein content was significant (Table 9). The mean protein content of the two parents was 48.48 and 44.00%, respectively. The midparent mean was 46.24% protein.

The range in protein content of the 94 F_2 plants was from 41.15 to 51.30%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 45.50% and contained 10 plants or 11% of the progeny. The F_2 mean was 46.68% which was significantly more than the midparent mean by .44% protein. There were 50 plants or 53% of the F_2's above the midparent mean while 44 plants or 47% of the F_2's were below that value. The median of this

F_2 population was 46.75%, and the midrange was 46.23. There were eight plants or 9% of the F_3's which exceeded the range of the high protein parent, F67-3673, and five plants or 5% which fell below the range of Bragg, the low protein parent.

There were three F_2 plants which fell below, but none exceeded two standard deviations from the F_2 mean.

The expected advance for the F_2 progeny was 3.52% protein. The F_2 mean of 46.68% protein plus the expected gain gave an expected mean of 50.20% protein in the next generation.

D67-6117

The frequency distributions for the F_2's and male lines having D67-6117 as the common female parent are presented in Table 17.

D67-6117 x F66-698

D67-6117 ranged in protein content from 47.87 to 50.57% while the range for F66-698 was from 48.94 to 50.64%. The mean protein content of D67-6117 and F66-698 was 48.96 and 49.62%, respectively. The mean midparent protein content was 49.24%.

The range in protein content of the 71 F_2 plants was from 43.45 to 52.25%. There was a moderately large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 51.00% and contained seven plants or 10% of the progeny. The F_2 mean was 48.86% which was .38% less protein than the midparent mean and was not significant. Thirty-eight plants or 54% of the F_2's fell

Table 17. Frequency distributions, means, and standard deviations for protein percent of D67-6117 x selected male parents and F_2's grown on Olivier silt loam, Baton Rouge, 1973.

Parents and generations[1]	Protein percent																									Protein content means[2]	s	Number of plants
	40	41	42	43		44		45		46		47		48		49		50		51		52		53				
D67-6117														1	4		2	1	1							48.96	.87	9
F66-698																2	4	1	2							49.62	.54	9
F_2					1			3	3	3	3	6	3	5	6	5	8	6	6	7	5		1			48.86	2.19	71
Midparent																										49.29		
D67-117														1	4		2	1	1							48.96	.87	9
F67-3673									1					1	2	1	3	1								48.48	1.39	9
F_2									1	3	8	11	8	8	5	7	8	12	5	5	3	1	1			48.70	1.66	86
Midparent																										48.72		
D67-117														1	4		2	1	1							48.96	.87	9
Tracy							2	1		4	2															45.66	.71	9
F_2			1			1	1	3	3	1	4	2	9	6	10	7	3	6	4	4			1			48.17	1.96	66
Midparent																										47.31		
D67-117														1	4		2	1	1							48.96	.87	9
Hutton						1		5	2		1															45.08	.69	9
F_2			1					2	3	7	4	8	1	2	5	4	3	2			2				1	47.63	2.17	45
Midparent																										47.07		
D67-6117														1	4		2	1	1							48.96	.87	9
Bragg				1	2	3	1	2																		43.89	.69	9
F_2			1		1	2	3	3	5	4	8	7	8	7	5	3	2	3	2		1	1				47.15	1.84	65
Midparent																										46.43		
D67-6117														1	4		2	1	1							48.96	.87	9
Pickett 71				1	1	2	2	1	1																	44.00	.86	9
F_2					3	1	3	2	4	2	2	2	4	6	2	4	1	1	1							46.45	2.13	43
Midparent																										46.48		

(Continued)

Table 17. Continued

Parents and generations[1]	Protein percent															Protein content means[2]	s	Number of plants
	40	41	42	43	44	45	46	47	48	49	50	51	52	53				
D67-6117									1	4	2	1	1			46.96	.87	9
Ransom			1	2	3	2										43.07	.93	9
F_2					2	1	5	2	3	1	5	4	4	4	5	2	2	2	1	1						46.04	2.17	44
Midparent																46.02		

1/Female parent listed first.
2/Protein in percent.

below the midparent mean while 33 plants or 47% of the F_2's were above that value. The median was 48.25% and the midrange was 47.85% of this F_2 population. There were 13 plants or 18% of the F_2's which surpassed the range of the high protein parent F66-698, and 22 plants or 31% which fell below the range of D67-6117, the lower protein parent.

There was one F_2 plant which fell below and none above two standard deviations of the F_2 mean.

The F_2 progeny had an expected advance of 3.47% protein. This figure added to the F_2 mean of 48.86% protein gave an expected mean of 52.33% protein.

D67-6117 x F67-3673

Protein content for D67-6117 ranged from 47.87 to 50.67% while F67-3673 ranged from 45.44 to 49.90%. The mean protein content of the two parents was 48.96 and 48.48%, respectively. The midparent mean was 48.72% protein.

The 86 F_2 plants ranged in protein content from 45.32 to 52.45%. The F_2 were continuously distributed and there were a large number of classes. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 47.00% which contained 11 plants or 13% of the progeny. The F_2 mean was 48.70% which was the same as the midparent mean. There were 42 plants or 49% of the F_2's which exceeded the midparent mean while 44 plants or 51% of the F_2's were below that value. Fifty-four plants or 63% of the F_2 progeny were within one standard deviation of the midparent mean while 85 plants or 99% fell within two standard deviations of the

midparent mean. This F_2 population had a median of 49.00% and a midrange of 48.89%. The range of the high protein parent, D67-6117, was exceeded by 10 plants or 9% of the F_2's, but no plants fell below the range of F67-3673, the lower protein parent.

There was one F_2 plant above and none below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 1.67% protein. This figure added to the F_2 mean of 48.70% protein gave an expected mean of 50.37% protein.

D67-6117 x Tracy

The range in protein content for D67-6117 was from 47.87 to 50.57% while the range for Tracy was from 44.61 to 46.27%. The mean protein content of the two parents were 48.96 and 45.66%, respectively. The midparent mean was 47.31% protein.

Protein content of the 66 F_2 plants ranged from 41.57 to 52.32%. There was a moderately large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 48.50% which contained 10 plants or 15% of the progeny. The F_2 mean was 48.17% which exceeded the midparent mean by .86% protein and was highly significant. There were 50 plants or 76% of the F_2's above the midparent mean and 16 plants or 24% of the F_2's were below that value. The median of this F_2 population was 47.50% and the midrange was 46.95%. There were 10 plants or 15% of the F_2's above the range of the high

protein parent, D67-6117, and two plants or 3% which fell below the range of the low protein parent, Tracy.

There was one F_2 plant above and two that fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.90% protein. The F_2 mean of 48.17% protein plus the 2.90% gave an expected F_3 mean of 51.07% protein.

D67-6117 x Hutton

D67-6117 ranged in protein content from 47.87 to 50.57% while Hutton ranged from 44.11 to 46.61%. The mean protein content of D67-6117 and Hutton was 48.96 and 45.08%, respectively. The mean midparent protein content was 47.07%.

The 45 F_2 plants ranged in protein content from 41.69 to 52.78%. There was a moderate number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 47.00% and contained seven plants or 16% of the progeny. The F_2 mean was 47.63% which had a significant .56% more protein than the midparent mean. There were 24 plants or 53% of the F_2's above the midparent mean while 21 plants or 47% of the F_2's were below that value. This F_2 population had a median of 47.75% and a midrange of 47.24%. There were three plants or 7% of the F_2's that exceeded the range of D67-6117, the high protein parent, and one plant or 2% which fell below the range of the low protein parent, Hutton.

There was one F_2 plant above and one that fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.22% protein. This figure added to the F_2 mean of 47.63% protein gave an expected F_3 mean of 50.95% protein.

D67-6117 x Bragg

The range in protein content for D67-6117 was from 47.87 to 50.57% and Bragg ranged from 42.67 to 44.77%. The difference in parents for protein content was significant (Table 9). The mean protein content of the two parents was 48.96 and 43.89%, respectively. The midparent mean was 46.43% protein.

Protein content of the 65 F_2 plants ranged from 41.83 to 51.75%. There was a moderately large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. There were two modal classes of eight plants each or 12% of the F_2 progeny which were 46.50 and 47.50%. The F_2 mean was 47.15% which was .72% more protein than the midparent mean and was highly significant. There were 43 plants or 66% of the F_2 plants above the midparent mean while 22 plants or 34% of the F_2's were below that value. The median was 47.25% and the midrange was 46.79% in this F_2 population. There were two plants or 3% of the F_2's which were above the range of D67-6117, the high protein parent, and one plant or 2% which fell below the range of the low protein parent, Bragg.

There was one F_2 plant above and one below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.66% protein. This figure added to the F_2 mean of 47.15% protein gave an expected mean of 49.81% protein.

D67-6117 x Pickett 71

Protein content for D67-6117 ranged from 47.87 to 50.57% while Pickett 71 ranged from 42.52 to 45.27%. The difference in parents for protein content was significant (Table 9). The mean protein content of D67-6117 and Pickett 71 was 48.96 and 44.00%, respectively. The mid-parent mean was 46.48% protein.

The 43 F_2 plants ranged in protein content from 43.07 to 50.32%. The F_2 were continuously distributed and there was a moderate number of classes. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 48.00% which contained six plants or 14% of the progeny. The F_2 mean was 46.45% which was essentially the same as the midparent mean. There were 22 plants or 51% of the F_2's above the midparent mean and 21 plants or 49% of the F_2's were below that value. Twenty-six plants or 61% of the F_2 progeny fell within one standard deviation of the midparent mean while all plants fell within two standard deviations of the midparent mean. This F_2 population had a median of 46.75% and a midrange of 46.70%. None of the F_2's fell outside the ranges of the two parents. However, this may have been due to the small F_2 population.

No F_2 plants fell outside the standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.15% protein. The F_2 mean of 46.45% protein plus the expected advance gave an expected mean of 49.60% protein for the F_3 generation.

D67-6117 x Ransom

D67-6117 ranged in protein content from 47.87 to 50.57% while Ransom ranged from 41.94 to 45.24%. The difference in parents for protein content was significant (Table 9). The mean protein content of the two parents was 48.96 and 43.07%, respectively. The mean midparent protein was 46.02%.

Protein content of the 44 F_2 plants ranged from 38.12 to 49.90%. There was a moderate number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. There were three modal classes of the F_2 progeny which were 44.00, 45.50, and 47.50% of which each contained five plants or 11% of the progeny. The F_2 mean was 46.04% which was the same as the midparent mean. Twenty-three plants or 53% of the F_2's were above the midparent mean while 20 plants or 47% of the F_2's were below that value. Thirty plants or 70% of the F_2 progeny fell within one standard deviation of the midparent mean, while all plants were within two standard deviations of the midparent mean. The median was 46.50% and the midrange was 44.01% for this F_2 population. None of the F_2's fell outside of the protein ranges of the two parents.

All F_2 plants were within two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.17% protein. This figure added to the F_2 mean of 46.04% protein gave an expected F_3 mean of 49.21% protein.

D68-4641

Presented in Table 18 are the frequency distributions for the F_2's and male lines having D68-4641 as a common female parent.

D68-4641 x F66-698

The range in protein content for D68-4641 was from 42.44 to 47.27% while the range for F66-698 was from 48.94 to 50.64%. The mean protein content of D68-4641 and F66-698 was 45.66 and 49.62%, respectively. The midparent mean was 47.64% protein.

The 100 F_2 plants ranged in protein content from 42.07 to 52.95%. There was a large number of classes and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 48.50% which contained 14 plants or 14% of the progeny. The F_2 mean was 47.62% which exceeded the midparent mean by .98% protein and was highly significant. There were 45 plants or 45% of the F_2's above the midparent mean while 55 plants or 55% of the F_2's were below that value. This F_2 population had a median of 48.25% and a midrange of 47.51%. There were 15 plants or 15% of the F_2's above the range of the high protein parent, F66-698, but none below the range of D68-4641, the low protein parent.

No F_2 plants surpassed, but three plants fell below two standard deviations of the F_2 mean.

Table 18. Frequency distributions, means, and standard deviations for protein percent of D68-4641 x selected male parents and F_2's grown on Olivier silt loam, Baton Rouge, 1973.

Parents and generations[1/]	Protein percent																										Protein content means[2/]	s	Number of plants
	38	39	40	41	42		43		44		45		46		47		48		49		50		51		52	53			
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
F66-698																			2	4	1	2					49.62	.54	9
F_2								2	1		2	3	4	6	2	13	8	14	7	5	10	8	8	3	3	1	48.62	2.12	100
Midparent																											47.64		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
F67-3673												1					1	2	1	3	1						48.48	.54	9
F_2									2			4	6	5	8	5	8	9	12	9	12	7	6	3	1	1	48.60	1.82	99
Midparent																											47.07		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
D67-6117																	1	4		2	1	1					48.96	.87	9
F_2					1	1	1				3	2	3	6	7	12	7	11	10	1	2	5	1	2	1		47.89	1.87	76
Midparent																											47.31		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
D69-0263									1			1					1		1		2	3					48.62	2.35	9
F_2	1				1			1	3		5	6	6	3	8	7	3	11	8	6	6	5	4	1		1	1	47.80	2.40	87
Midparent																											47.14		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
Hutton									1		5	2		1													45.08	.69	9
F_2							1	2	4	3	5	6	5	9	12	13	10	8	5	4	2		1				47.03	1.67	90
Midparent																											45.37		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
Pickett 71						1	1	1	2	2	1	1															44.00	.86	9
F_2					1		2	2	4	3	8	8	3	7	16	8	8	6	15	6	1						46.97	1.82	98
Midparent																											44.83		

(Continued)

Table 18. Continued

Parents and generations[1]	Protein percent																										Protein content means[2]	s	Number of plants
	38	39	40	41	42		43		44		45		46		47		48		49		50		51		52	53			
D48-4641						1				1		1	2	2	1	1											45.66	1.44	9
Bregg							1	2	3	1	2																43.89	.69	9
F_2					1	2		4	4	1	5	8	8	9	6	7	10	7	1	2	1	3					46.64	1.87	79
Midparent																											44.78		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
Tracy										2	1		4	2													45.66	.71	9
F_2				1	2	1	3	5	8	12	8	9	11	13	8	5	2										45.49	1.49	93
Midparent																											45.66		
D68-4641						1				1		1	2	2	1	1											45.66	1.44	9
Ransom					1	2	3	2				1															43.07	.93	9
F_2			1	1	1	2	5	6	11	14	11	13	11	10	7	4	4	3									45.23	1.61	104
Midparent																											44.37		

1/Female parent listed first.
2/Protein in percent.

The expected advance for the F_2 progeny was 3.08% protein. This figure added to the F_2 mean of 48.62% protein will give an expected mean for the F_3 population of 51.70% protein.

D68-4641 x F67-3673

Protein content for D68-4641 ranged from 42.44 to 47.24% while the range for F67-3673 was from 45.44 to 49.90%. The mean protein content of the two parents was 45.66 and 48.48%, respectively. The mean midparent protein was 47.07%.

The range in protein content of the 99 F_2 plants was from 43.82 to 52.32%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The two modal classes of the F_2 progeny were 49.00 and 50.00% which contained 12 plants each or 12% of the progeny. The F_2 mean was 48.60% which was 1.53% more protein than the midparent mean and was highly significant. There were 73 plants or 74% of the F_2's above the midparent mean while 27 plants or 26% of the F_2's were below that value. The median of this F_2 population was 48.75% and the midrange was 48.07%. There were 18 plants or 18% of the F_2's which were above the range of F67-3673, the high protein parent, but there were none below the range of the low protein parent, D68-4641.

There was one F_2 plant above and two below two standard deviations of the F_2 mean.

The F_2 progeny had an expected advance of 1.28% protein. The 1.28% protein added to the F_2 mean of 48.60% protein gave an F_3 expected mean of 49.88% protein.

D68-4641 x D67-6117

The D68-4641 ranged in protein content from 42.44 to 47.24% while D67-6117 ranged from 47.87 to 50.57%. The mean protein content of the two parents was 45.66 and 48.96%, respectively. The midparent mean was 47.31% protein.

Protein content of the 76 F_2 plants ranged from 42.24 to 51.88%. The F_2 were continuously distributed and there was a moderately large number of classes. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 47.50% which contained 12 plants or 16% of the progeny. The F_2 mean was 47.89% which was .58% more protein than the midparent mean and highly significant. There were 46 plants or 61% of the F_2's which surpassed the midparent mean while 30 plants or 39% of the F_2's were below that value. The median was 47.75% and the midrange was 47.06% for this F_2 population. Four plants or 5% of the F_2's were above the range of the high protein parent, D67-6117, and one plant or 1% below the range of D68-4641, the low protein parent.

One F_2 plant exceeded and three plants were below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.11% protein. The expected advance added to the F_2 mean of 47.89% protein gave an F_3 expected mean of 50.00% protein.

D68-4641 x D69-0263

Protein content for D68-4641 ranged from 42.44 to 47.24% while the range for D69-0263 was from 43.94 to 50.57%. The mean protein content of D68-4641 and D69-0263 was 45.66 and 48.62%, respectively. The midparent mean was 47.14% protein.

The 87 F_2 plants ranged in protein content from 38.25 to 53.21%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 48.50% which contained 11 plants or 13% of the progeny. The F_2 mean was 47.14% which surpassed the midparent mean by .66% protein and was highly significant. There were 53 plants or 61% of the F_2's above the midparent mean while 34 plants or 39% of the F_2's were below that value. This F_2 population had a median of 47.75% and a midrange of 45.73%. Seven plants or 8% of the F_2's exceeded the range of D69-0263, the high protein parent, and two plants or 2% were below the range of the low protein parent, D68-4641.

There was one F_2 plant above and one below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 1.73% protein. The F_2 mean of 47.80% protein plus the expected advance gave an expected mean of 49.53% protein.

D68-4641 x Hutton

The range in protein content for D68-4641 was from 42.44 to 47.24% while Hutton ranged from 44.11 to 46.61%. The mean protein content of the two parents was 45.66 and 45.08%, respectively. The midparent mean was 45.37% protein.

Ninety F_2 plants ranged in protein content from 43.00 to 51.20%. The F_2 were continuously distributed and there was a large number of classes. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 47.50% which contained 13 plants or 14% of the progeny. The F_2 mean was 47.03% which exceeded the midparent mean by 1.66% protein and was highly significant. There were 80% or 72 plants of the F_2's which fell above the midparent mean while 20% or 18 plants of the F_2's were below that value. The median for this F_2 population was 46.75% and the midrange was 47.10%. There were 30 plants or 33% of the F_2's above the range of the high protein parent, D67-4641, but none below the range of Hutton, the lower protein parent.

There was one F_2 plant above and one plant that fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 1.90% protein. This figure added to the F_2 mean of 47.03% protein gave an expected F_3 mean of 48.93% protein.

D68-4641 x Pickett 71

The range in protein content for D68-4641 was from 42.44 to 47.24% while Pickett 71 ranged from 42.52 to 45.27%. The mean protein content of D68-4641 and Pickett 71 was 45.66 and 44.00%, respectively. The midparent mean was 44.83% protein.

Protein content of the 98 F_2 plants ranged from 41.75 to 50.22%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 47.00% which contained 16 plants or 16% of the progeny. The F_2 mean was 46.97% which was 2.14% more protein than the midparent mean and highly significant. There were 74 plants or 76% of the F_2's which surpassed the midparent mean and 24 plants or 24% of the F_2's were below that value. This F_2 population had a median of 46.25% and a midrange of 45.99%. There were 36 plants or 37% of the F_2's above the range of D68-4641, the high protein parent, and one plant or 1% below the range of the high protein parent, Pickett 71.

No F_2 plants were above but there was one plant below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.02% protein. This figure added to the F_2 mean of 46.97% protein gave an expected mean for the next generation of 48.99% protein.

D68-4641 x Bragg

D68-4641 ranged in protein content from 42.44 to 47.24% while the range for Bragg was from 42.67 to 44.77%. The mean protein content of the two parents was 45.66 and 43.89%, respectively. The midparent mean was 44.78% protein.

The 79 F_2 plants ranged in protein content from 42.24 to 50.67%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 48.00% which contained 10 plants or 13% of the progeny. The F_2 mean was 46.64% which was highly significant to the midparent mean and exceeded it by 1.86% protein. There were 65 plants or 82% of the F_2's above the midparent mean while 14 plants or 17% of the F_2's were below that value. The median of this F_2 population was 46.50% and the midrange was 46.64%. Twenty-four plants or 30% of the F_2's were above the range of D68-4641, the high protein parent, and one plant or 1% was below the range of the low protein parent, Bragg.

One F_2 plant was above and three plants were below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.37% protein. The F_2 mean of 46.64% protein plus the 2.37% gave an expected mean of 49.01% protein.

D68-4641 x Tracy

The protein content for D68-4641 ranged from 42.44 to 47.24% while the range for Tracy was from 44.61 to 46.27%. D68-4641 and Tracy had the same mean protein content of 45.66%. Also, the midparent mean was 45.66% protein.

Protein content of the 93 F_2 plants ranged from 41.42 to 48.20%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 46.50% and contained 13 plants or 14% of the progeny. The F_2 mean was 45.49% which was only .17% less protein than the midparent mean and was not significant. There were 39 plants or 42% of the F_2's which exceeded the midparent mean and 54 plants or 58% of the F_2's were below that value. This F_2 population's median was 44.75% and its midrange was 44.81%. Two plants or 2% of the F_2's surpassed the range of D68-4641, the female parent, and three plants or 3% were below the range of D68-4641. The range of Tracy was completely included within the range of D68-4641 in the frequency distribution table.

No F_2 plants were above but one plant fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 1.42% protein and when added to the F_2 mean of 45.49% protein gave an expected F_3 mean of 46.91% protein.

D68-4641 x Ransom

The range in protein content for D68-4641 was from 42.44 to 47.24% while Ransom ranged from 41.94 to 45.24%. The mean protein content of the two parents was 45.66 and 43.03%, respectively. The mean midparent protein was 44.37%.

Protein content of the 104 F_2 plants ranged from 40.07 to 48.72%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 44.50% which contained 14 plants or 14% of the progeny. The F_2 mean was 45.23% or .86% higher in protein than the midparent mean and highly significant to it. There were 69% or 72 plants of the F_2's which exceeded the midparent mean while 32 plants or 31% of the F_2's were below the midparent. The median of this F_2 population was 44.75% and the midrange was 44.40%. Seven plants or 7% of the F_2's were above the range of D68-4641, the high protein parent, and two plants or 2% were below the range of the low protein parent, Ransom.

One F_2 plant was above two standard deviations of the F_2 mean, but none were below that level.

The expected advance for the F_2 progeny was only .26% protein. The F_2 mean of 45.23% protein plus the .26% gave an expected mean of 45.49% protein for the F_3 generation.

F66-698

Presented in Table 19 are the frequency distributions of the F_2's and male lines having F66-698 as a common female parent.

F66-698 x Ransom

The protein content for F66-698 ranged from 48.94 to 50.64% while the range for Ransom was from 41.94 to 45.24%. The difference in parents for protein content was significant (Table 9). The mean protein content of F66-698 and Ransom was 49.62 and 43.07%, respectively. The midparent mean was 46.35% protein.

The 37 F_2 plants ranged in protein content from 42.87 to 51.24%. There was a small number of classes due to the small population, but the F_2 plants appeared to be continuously distributed for protein. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 49.50% and contained nine plants or 24% of the progeny. The F_2 mean was 49.14% which exceeded the midparent mean by 2.79% protein and was highly significant. Thirty-six plants or 97% of the F_2's surpassed the midparent mean while only one plant or 3% of the F_2's were below that value. The median was 48.75% and the midrange was 47.06% for this F_2 population. Four plants or 11% of the F_2's were above the range of F66-698, the high protein parent, and none below the range of the low protein parent, Ransom.

No F_2 plants were above, but one plant was below two standard deviations of the F_2 mean.

Table 19. Frequency distributions, means, and standard deviations for protein percent of F66-698 and Pickett 71 x selected male parents and F_2's grown on Olivier silt loam, Baton Rouge, 1973.

Parents and generations[1/]	Protein percent																									Protein content means[2/]	s	Number of plants
	40	41	42		43		44		45		46		47		48		49		50		51		52		53				
F66-698																	2	4	1	2						49.62	.54	9
Ransom			1	2	3	2				1																43.07	.93	9
F_2					1								1	1	2	6	5	9	6	2	4					49.14	1.19	37
Midparent																										46.35		
F66-698																	2	4	1	2						49.62	.54	9
Hutton							1		5	2		1														45.08	.69	9
F_2		1						2		3	5	3	8	7	5	14	10	7	8	5	3	1		1		48.31	1.90	83
Midparent																										47.35		
F66-698																	2	4	1	2						49.62	.54	9
Tracy								2	1		4	2														45.66	.71	9
F_2								1	2		3	11	12	12	19	8	7	2	2		1					47.70	1.13	80
Midparent																										47.64		
F66-698																	2	4	1	2						49.62	.54	9
Pickett 71				1	1	1	2	2	1	1																44.00	.86	9
F_2			1	1		1	2	1	4	5	12	5	5	4	3	6	2				1					46.43	1.68	52
Midparent																										46.81		
F66-698																	2	4	1	2						49.62	.54	9
Bragg					1	2	3	1	2																	43.89	.69	9
F_2				1	4	3	4	2	8	7	11	11	7	7	2	1		3	2							46.06	1.67	73
Midparent																										46.76		
Pickett 71				1	1	1	2	2	1	1																44.00	.86	9
Hutton							1		5	2		1														45.08	.69	9
F_2		1		1	2	5	2	5	2	2	4	2	1	2	1				1	1						45.23	2.05	32
Midparent																										44.54		

(Continued)

Table 19. Continued

Parents and generation[1]	Protein percent																		Protein content means[2]	s	Number of plants
	40	41	42	43		44		45	46		47	48	49	50	51	52	53				
Pickett 71				1	1	1	2	2	1	1									44.00	.86	9
Ransom			1	2	3	2				1									43.07	.93	9
F_2			1	6	4	5	7	5	3	6	5	1	1	2			1			44.15	1.66	47
Midparent																				43.54		

1/Female parent listed first.
2/Protein in percent.

The F_2 progeny expected advance was 1.34% protein and when added to the F_2 mean of 49.14% protein gave an expected F_3 mean of 50.48% protein.

F66-698 x Hutton

F66-698 ranged in protein content from 48.94 to 50.64% and Hutton ranged from 44.11 to 46.61%. The mean protein content of the two parents was 49.62 and 45.08%, respectively. The mean midparent protein was 47.35%.

Protein content of the 83 F_2 plants ranged from 41.67 to 52.62%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 48.50% and contained 14 plants or 17% of the progeny. The mean of the F_2 was 48.31% which exceeded the midparent mean by .96% protein and was highly significant. There were 57 plants or 69% of the F_2's which surpassed the midparent mean while 26 plants or 31% of the F_2's were below that value. This F_2 population's median was 48.25% and its midrange was 47.15%. Five plants or 6% of the F_2's were above the range of F66-698, the high protein parent, and one plant or 1% which fell below the range of the low protein parent, Hutton.

One F_2 plant was above and one plant fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.01% protein. This figure added to the F_2 mean of 48.31% protein gave an expected mean of 51.32% protein.

F66-698 x Tracy

The range in protein content for F66-698 was from 48.94 to 50.64% while Tracy ranged from 44.61 to 46.27%. The mean protein content of the two parents were 49.62 and 44.66%, respectively. The midparent mean was 47.64% protein.

The 80 F_2 plants ranged in protein content from 44.57 to 50.75%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 48.00% which contained 19 plants or 24% of the progeny. The F_2 mean was 47.70% which was essentially the same as the midparent mean. There were 49% or 39 plants of the F_2's which surpassed the midparent mean and 41 plants or 51% of the F_2's were below that value. Sixty plants or 75% of the F_2 progeny had a protein content within one standard deviation of the midparent mean while 75 plants or 94% were within two standard deviations of the midparent mean. The median of this F_2 population was 47.75% and the midrange was 47.66%. One plant or 1% of the F_2's exceeded the range of the high protein parent, F66-698, but no plants were below the range of Tracy, the low protein parent.

There was one F_2 plant above and three plants below two standard deviations of the F_2 mean.

The F_2 progeny expected advance was 1.39% protein and when added to the F_2 mean of 47.70% protein gave an expected F_3 mean of 49.09% protein.

F66-698 x Pickett 71

F66-698 ranged in protein content from 48.94 to 50.64% while Pickett 71 ranged from 42.52 to 45.27%. The difference in parents for protein content was significant (Table 9). The mean protein content of F66-698 and Pickett 71 was 49.62 and 44.00%, respectively. The mid-parent mean was 46.81% protein.

The protein content of the 52 F_2 plants ranged from 42.18 to 50.90%. There was a moderate number of classes and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 46.00% which contained 12 plants or 23% of the progeny. The F_2 mean was 46.43% which was .38 less protein than the midparent mean, but was not significant. Twenty-four plants or 46% of the F_2's exceeded the midparent mean while 28 plants or 54% of the F_2's were below that value. There was one plant or 2% of the F_2's above the range of the high protein parent, F66-698, and one plant or 2% below the range of Pickett 71, the low protein parent.

One F_2 plant was above and two plants were below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.48% protein. This figure added to the F_2 mean of 46.43% protein gave an expected mean of 48.91% protein.

F66-698 x Bragg

Protein content of F66-698 ranged from 48.94 to 50.64% and the range for Bragg was from 42.67 to 44.77%. The difference in the parents for protein content was significant (Table 9). The mean protein content of the two parents was 49.62 and 43.89%, respectively. The mean midparent protein was 46.76%.

The 72 plants ranged in protein content from 42.41 to 50.12%. There was a large number of classes and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. Two modal classes occurred in the F_2 progeny at 46.00 and 46.50% and each contained 11 plants or 15% of the progeny. The F_2 mean was .70% protein below the midparent mean of 46.76% and was highly significant. The midparent mean was exceeded by 22 plants or 30% of the F_2's while 51 plants or 70% of the F_2's were below that value. The median was 46.00% and the midrange was 46.27% for this F_2 population. None of the F_2's was above the range of F66-698, the high protein parent, but one plant or 1% was below the range of the low protein parent, Bragg.

Two F_2 plants surpassed and one plant was below two standard deviations of the F_2 mean.

The F_2 progeny had an expected advance of 2.56% protein and when added to the F_2 mean of 46.06% protein gave an expected F_3 mean of 48.62% protein.

Pickett 71

Frequency distributions of the F_2's and male lines having Pickett 71 as a common female parent are presented in Table 19.

Pickett 71 x Hutton

Protein content for Pickett 71 ranged from 42.52 to 45.27% while the range for Hutton was from 44.11 to 46.61%. The mean protein content of Pickett 71 and Hutton was 44.00 and 45.08%, respectively. The midparent mean was 44.54% protein.

Protein content of the 32 F_2 plants ranged from 40.87 to 50.62%. There was a small number of classes because of the small population, but the protein content of the F_2 plants appeared to be continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny had two modal classes which were 43.50 and 44.50% and each contained five plants or 16% of the progeny. The F_2 mean was 45.23% which significantly exceeded the midparent mean by .69% protein. Eighteen plants or 56% of the F_2's were above the midparent mean and 14 plants or 44% of the F_2's were below that value. This F_2 population's median was 45.50% and its midrange was 45.75%. Six plants or 19% of the F_2's were above the range of the high protein parent, Hutton, and one plant or 3% was below the range of Pickett 71, the low protein parent.

Two F_2 plants surpassed two standard deviations of the F_2 mean for protein and one plant was below this level.

The expected advance for the F_2 progeny was 3.10% protein. This figure added to the F_2 mean of 45.23% protein gave an F_3 expected mean of 48.33% protein.

Pickett 71 x Ransom

Pickett 71 ranged in protein content from 42.52 to 45.27% and the range for Ransom was from 41.94 to 45.24%. The mean protein content of Pickett 71 and Ransom was 44.00 and 43.07%, respectively. The midparent mean was 43.54% protein.

Protein content of the 47 F_2 plants ranged from 41.59 to 49.68%. There was a moderate number of classes and the F_2 plants were continuously distributed. The F_2 progeny modal class was 43.50% which contained seven plants or 15% of the progeny. The F_2 mean was 44.15% which was .61% more protein than the midparent mean and was highly significant. There were 27 plants or 57% of the F_2's which exceeded the midparent mean while 20 plants or 43% of the F_2's were below that value. The F_2 population median was 44.50% and the midrange was 45.64%. There were six plants or 13% of the F_2's above the range of Pickett 71, the high protein parent, and one plant or 2% below the range of the lower protein parent, Ransom.

One F_2 plant exceeded the F_2 mean by more than two standard deviations.

The expected advance for the F_2 progeny was 2.07% protein. The F_2 mean of 44.15% protein plus the expected advance gave an expected mean of 46.22% protein in the F_3 generation.

Tracy

In Table 20, frequency distributions are presented of the F_2's and male lines having Pickett 71 as a common female parent.

Tracy x Pickett 71

Protein content for Tracy ranged from 44.61 to 46.27% while the range for Pickett 71 was from 42.52 to 45.27%. The mean protein content of the two parents was 45.66 and 44.00%, respectively. The midparent mean was 44.83% protein.

The F_2 plants ranged in protein content from 41.25 to 48.85%. There was a large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 45.50% which contained 16 plants or 21% of the progeny. The F_2 mean was 45.19% which was significantly more than the midparent mean by .36% protein. There were 45 plants or 59% of the F_2's which had a higher percent protein than the midparent mean while 31 plants or 41% of the F_2's were below that value. The median was 45.50%, and the midrange was 45.05% for this F_2 population. Ten plants or 13% of the F_2's were above the range of Tracy, and the high protein parent and two plants or 3% which fell below the range of the lower protein parent, Pickett 71.

Three F_2 plants exceeded and two plants were below two standard deviations of the F_2 mean.

Table 20. Frequency distributions, means, and standard deviations for protein percent of Tracy, Hutton, and Bragg x selected male parents and F_2's grown on Olivier silt loam, Baton Rouge, 1973.

Parents and generation[1/]	Protein percent																									Protein content means[2/]	s	Number of plants
	39	40	41	42		43			44		45		46		47		48		49	50	51	52	53					
Tracy										2	1		4	2												45.66	.71	9
Pickett 71						1	1	1	2	2	1	1														44.00	.86	9
F_2				2		1	2	8	6	7	9	16	8	7	4	2	1	2	1							45.19	1.50	76
Midparent																										44.83		
Tracy										2	1		4	2												45.66	.71	9
Hutton									1		5	2		1												45.08	.69	9
F_2		1	2	1	1	1	2	4	4	9	9	13	10	12	10	5	7	2								45.64	1.69	93
Midparent																										45.37		
Tracy										2	1		4	2												45.66	.71	9
Bragg							1	2	3	1	2															43.89	.69	9
F_2						1	5	2	2	2	2	1	2	3	2	1										44.87	1.61	23
Midparent																										44.78		
Tracy										2	1		4	2												45.66	.71	9
Ransom					1	2	3	2			1															43.07	.93	9
F_2	2	1			4	4	10	11	13	5	6	10	8	3		1										44.12	1.56	78
Midparent																										44.37		
Hutton									1		5	2		1												45.08	.69	9
Ransom					1	2	3	2				1														43.07	.93	9
F_2			2	1	4	4	7	6	3	7	4	1	6		1	1		1		1						44.02	1.89	49
Midparent																										44.08		
Bragg							1	2	3	1	2															43.89	.69	9
Hutton									1		5	2		1												45.08	.69	9
F_2			1	2	1	1	5	7	4	10	6	11	7	4	3	1	1									44.78	1.48	64
Midparent																										44.49		

(Continued)

Table 20. Continued

Parents and generation[1]	Protein percent																	Protein content means[2]	s	Number of plants
	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53					
Bragg					1	2	3	4	2									43.89	.69	9
Pickett 71					1	1	2	2	1	1								44.00	.86	9
F_2				1	3		2	2		1			1					44.41	2.15	10
Midparent																		43.95		
Bragg					1	2	3	4	2									43.89	.69	9
Ransom				1	2	3	2			1								43.07	.93	9
F_2		1		2	2	5	6	6	6	11	2	4	3	2	2	1	1	44.22	1.66	54
Midparent																		43.48		

1/Female parent listed first.
2/Protein in percent.

The expected advance for the F_2 progeny was 1.93% protein. This figure added to the F_2 mean of 45.19% protein gave an expected F_3 mean of 47.12% protein.

Tracy x Hutton

Tracy ranged in protein content from 44.61 to 46.27% while the range for Hutton was from 44.11 to 46.61%. The mean protein content of Tracy and Hutton was 45.66 and 45.08%, respectively. The midparent mean was 45.37% protein.

The range in protein content of the 93 F_2 plants was from 40.13 to 48.33%. There was a large number of classes and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 45.50% and contained 13 plants or 14% of the progeny. The F_2 mean was 45.64% which was .27% more protein than the midparent mean but was not significant. There were 52 plants or 56% of the F_2's which surpassed the midparent mean while 41 plants or 44% of the F_2's were below that value. The median of the F_2 population was 44.50%, and the midrange was 44.23%. Twenty-four plants or 26% of the F_2's were above the range of the high protein parent, Tracy, and 12 plants or 13% were below the range of Hutton, the lower protein parent.

No F_2 plants were above, but there were five plants that fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.47% protein and when added to the F_2 mean of 45.64% protein gave an expected F_3 mean of 48.11% protein.

Tracy x Bragg

The range in protein content for Tracy was from 44.61 to 46.27% while Bragg ranged from 42.67 to 44.77%. The mean protein content of the two parents was 45.66 and 43.89%, respectively. The mean midparent protein was 44.78%.

Protein content of the 23 F_2 plants ranged from 42.25 to 47.58%. There was a small number of classes due to the small population, but the F_2 plants appeared to be continuously distributed for protein. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 43.00% which contained five plants or 22% of the progeny. The F_2 mean was 44.87% which was about the same as the midparent mean (.09% more). There were 10 plants or 43% of the F_2's above the midparent mean while 13 plants or 57% of the F_2's were below that value. The median was 45.00%, and the midrange was 44.92% for this F_2 population. Three plants or 13% of the F_2's exceeded the range of Tracy, the high protein parent, and one plant or 4% fell below the range of the low protein parent, Bragg.

All F_2 plants were within two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.30% protein. The expected advance plus the F_2 mean of 44.87% protein gave an expected mean of 47.17% protein for the F_3 generation.

Tracy x Ransom

Protein content for Tracy ranged from 44.61 to 46.27% while the range for Ransom was from 41.94 to 45.24%. The mean protein content of Tracy and Ransom was 45.66 and 43.07%, respectively. The mean of the two parents was 44.37% protein.

The 78 F_2 plants ranged in protein content from 39.57 to 47.25%. There was a moderately large number of classes, and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 44.00% and contained 13 plants or 17% of the progeny. The F_2 mean was 44.12% which was not significantly less than the midparent mean. There were 31 plants or 40% of the F_2's above the midparent mean while 47 plants or 60% of the F_2's were below that value. In this F_2 population, the median was 44.00%, and the midrange was 43.41%. The range of the high protein parent, Tracy, was exceeded by one or 1% of the F_2 plants and three plants or 4% were below the range of the lower protein parent, Ransom.

There was one F_2 plant which surpassed and three that fell below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.00% protein. This figure added to the F_2 mean of 44.12% protein gave an expected F_3 mean of 46.12% protein.

Hutton

The frequency distribution of the parental lines and F_2 from the cross of Hutton x Ransom is presented in Table 20.

Hutton ranged in protein content from 44.11 to 46.61% while the range for Ransom was from 41.94 to 45.24%. The mean protein content of the two parents was 45.08 and 43.07%, respectively. The midparent mean was 44.08% protein.

Protein content of the 49 F_2 plants ranged from 40.54 to 49.51%. There was a moderate number of classes and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The bimodal classes of the F_2 progeny were 43.00 and 44.50% and each contained seven plants or 14% of the progeny. The F_2 mean was 44.02% which was essentially the same as the midparent mean. The midparent mean was exceeded by 23 plants or 47% of the F_2's while 26 plants or 53% of the F_2's were below that value. The median of this F_2 population was 44.50%, and the midrange was 45.03%. Four plants or 8% of the F_2's were above the range of the high protein parent, Hutton, and three plants or 6% were below the range of Ransom, the lower protein parent.

Two F_2 plants surpassed two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.73% protein. The F_2 mean of 44.02% protein plus the 2.73% gave an expected mean of 46.75% protein for the F_3 generation.

Bragg

In Table 20, frequency distributions are presented for the F_2's and male lines having Bragg as a common female parent.

Bragg x Hutton

The range in protein content for Bragg was from 42.67 to 44.77% while Hutton ranged from 44.11 to 46.61%. The mean protein content of Bragg and Hutton was 43.89 and 45.08%, respectively. The mean midparent protein was 44.49%.

Protein content of the 64 F_2 plants ranged from 41.07 to 48.08%. There was a moderate number of classes and the F_2 were continuously distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The F_2 progeny modal class was 45.50% and contained 11 plants or 17% of the progeny. The F_2 mean was 44.78% which exceeded the midparent mean by .29% protein but was not significant. There were 38 plants or 59% of the F_2's above the midparent mean while 26 plants or 41% of the F_2's were below that value. The median of the F_2 population was 44.50%, and the midrange was 44.58%. There were five plants or 8% of the F_2's above the range of the high protein parent, Hutton, and five plants or 8% below the range of Bragg, the lower protein parent.

There were two F_2 plants above and three below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.06% protein. This figure added to the F_2 mean of 44.78% protein gave an F_3 expected mean of 46.84% protein.

Bragg x Pickett 71

Bragg ranged in protein content from 42.67 to 44.77% while the range for Pickett 71 was from 42.52 to 45.27%. The range of Bragg was completely included within the range of Pickett 71. The mean protein content of the two parents were 43.89 and 44.00%, respectively. The midparent mean was 43.95% protein.

The range in protein content of the 10 F_2 plants was from 42.07 to 49.88%. The population was very small and so was the number of classes. The modal class could not be determined properly as a result of the very few F_2 progeny. It was surprising that the F_2 mean of 44.41% was fairly close to the midparent mean of 43.95. Also, it was interesting to note that there was one F_2 plant above the range of Pickett 71 and one F_2 plant below the range of Pickett 71.

There was also one F_2 plant which exceeded two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 3.29% protein. The F_2 mean of 44.41% protein plus the expected advance would give an expected mean of 47.70% protein in the F_3 generation.

Bragg x Ransom

The range in protein content for Bragg was from 42.67 to 44.77% while Ransom ranged from 41.94 to 45.24%. The mean protein content of the two parents was 43.89 and 43.07%, respectively. The midparent mean was 43.48% protein.

The 54 F_2 plants ranged in protein content from 40.29 to 48.35%. There was a moderate number of classes, and the F_2 were continuously

distributed. There were some components of the distribution which caused it to be partially different from a normally distributed quantitative character. The modal class of the F_2 progeny was 44.50% and contained 11 plants or 20% of the progeny. The F_2 mean was 44.22% which was .74% more protein than the midparent mean and was highly significant. There were 35 plants or 65% of the F_2's above the midparent mean while 19 plants or 35% of the F_2's were below that value. The median was 44.50% and the midrange was 44.32%. Nine plants or 17% of the F_2's exceeded the range of Bragg, the high protein parent and three plants or 6% were below the range of the lower protein parent, Ransom.

There were two F_2 plants above and one below two standard deviations of the F_2 mean.

The expected advance for the F_2 progeny was 2.25% protein. This figure added to the F_2 mean of 44.22% protein gave an expected mean of 46.47%.

Table 21 shows the range, mean, heritabilities, expected advance, and predicted mean for each frequency distribution. The expected genetic advance was calculated with the intent of selecting the highest 10% of the progeny. The expected advance is especially useful to plant breeders as a prediction of advance of a population mean by selection. The progeny of three crosses, all high protein x high protein crosses, had an F_3 predicted mean of over 52% protein (Table 21).

The phenotypic correlation coefficients between all combinations of characters studied for the parents and F_2 populations are presented in Table 22. The correlation coefficients were as follows between:

Table 21. Heritability estimate, expected advance, mean, predicted population mean and range for protein in the F_2 soybean populations grown on Olivier silt loam, Baton Rouge, 1973.

Cross combination	Heritability	G_s [1/]	Mean	Predicted Mean	Range
D69-0263 x F66-698	.71 [2/]	2.64 [2/]	49.78	52.42 [2/]	45.30-52.46
D69-0263 x D67-6117	[2/]	[2/]	49.63	[2/]	48.79-51.00
D69-0263 x Tracy	.32	.88	49.12	50.00	45.00-51.33
D69-0263 x F67-3673	.19	.67	47.74	48.41	43.65-51.60
D69-0263 x Hutton	.63	2.31	47.17	49.48	40.95-52.48
D69-0263 x Bragg	.64	2.39	46.96	49.35	41.91-51.13
D69-0263 x Pickett 71	.60	2.38	46.92	49.30	40.38-52.00
D69-0263 x Ransom	.59	2.40	45.80	48.20	41.27-49.59
F67-3673 x F66-698	.85	3.43	48.89	52.32	44.55-52.42
F67-3673 x Tracy	.74	2.55	47.87	50.42	41.24-51.50
F67-3673 x Hutton	.80	3.07	47.22	50.29	40.99-51.55
F67-3673 x Ransom	.77	3.18	46.75	49.93	41.92-50.25
F67-3673 x Bragg	.75	2.57	46.58	49.15	42.58-51.37
F67-3673 x Pickett 71	.81	3.52	46.68	50.20	41.15-51.30
D67-6117 x F66-698	.90	3.47	48.86	52.33	43.45-52.25
D67-6117 x F67-3673	.57	1.67	48.70	50.37	45.32-52.45
D67-6117 x Tracy	.84	2.90	48.17	51.07	41.57-52.32
D67-6117 x Hutton	.87	3.22	47.63	50.95	41.69-52.78
D67-6117 x Bragg	.82	2.66	47.15	49.81	41.83-51.75
D67-6117 x Pickett 71	.84	3.15	46.45	49.60	43.07-50.32
D67-6117 x Ransom	.83	3.17	46.04	49.21	38.12-49.90
D68-4641 x F66-698	.83	3.08	48.62	51.70	42.07-52.95
D68-4641 x F67-3673	.40	1.28	48.60	49.88	43.82-52.32
D68-4641 x D67-6117	.64	2.11	47.89	50.00	42.24-51.88

(Continued)

Table 21. Continued

Cross combination	Heritability	G_s 1/	Mean	Predicted mean	Range
D68-4641 x D69-0263	.41	1.73	47.80	49.53	38.25-53.21
D68-4641 x Hutton	.65	1.90	47.03	48.93	43.00-51.20
D68-4641 x Pickett 71	.63	2.02	46.97	48.99	41.75-50.22
D68-4641 x Bragg	.72	2.37	46.64	49.01	42.24-50.67
D68-4641 x Tracy	.54	1.42	45.49	46.91	41.42-48.20
D68-4641 x Ransom	.09	.26	45.23	45.49	40.07-48.72
F66-698 x Ransom	.64	1.34	49.14	50.48	42.87-51.24
F66-698 x Hutton	.90	3.01	48.31	51.32	41.67-52.62
F66-698 x Tracy	.70	1.39	47.70	49.09	44.57-50.75
F66-698 x Pickett 71	.84	2.48	46.43	48.91	42.18-50.90
F66-698 x Bragg	.87	2.56	46.06	48.62	42.41-50.12
Pickett 71 x Hutton	.86	3.10	45.23	48.33	40.87-50.62
Pickett 71 x Ransom	.71	2.07	44.15	46.22	41.59-49.68
Tracy x Pickett 71	.73	1.93	45.19	47.12	41.25-48.85
Tracy x Hutton	.83	2.47	45.64	48.11	40.13-48.33
Tracy x Bragg	.81	2.30	44.80	47.17	42.25-47.58
Tracy x Ransom	.73	2.00	44.12	46.12	39.57-47.25
Hutton x Ransom	.82	2.73	44.02	46.75	40.54-49.51
Bragg x Hutton	.79	2.06	44.78	46.84	41.07-48.08
Bragg x Pickett 71	.87	3.29	44.41	47.70	42.07-49.88
Bragg x Ransom	.77	2.25	44.22	46.47	40.29-48.35

1/Expected genetic advance calculated for a 10% selection differential.
2/These figures were not calculated because only 4 F_2 plants were grown.

Table 22. Phenotypic correlation coefficients between all selected characters for parents and F_2 populations grown on Olivier silt loam, Baton Rouge, 1973.

Selected characters	Maturity date	Plant height	H.L.P.[1/]	Yield	Protein content
Flowering date	.42**	.34**	.17**	-.07	.21**
Maturity date		.36**	.04	.11*	.03
Plant height			.21**	.13**	.26**
H.L.P.[1/]				-.24**	.06
Yield					-.07

*P 0.05 **P 0.01

1/Height of lower pod.

1) protein and the characters flowering date and plant height were both positive and highly significant, but the associations were low; 2) maturity date and the characters flowering date and plant height were both positive, highly significant, but were moderately low in association; 3) maturity date and yield had a low but highly significant positive association; 4) plant height and the characters flowering date, height of lower pod, and yield were all positive, highly significant and were moderately low to low in association; 5) height of lower pod and plant height had a low positive association; 6) height of lower pod and yield was negatively associated and highly significant but the association was moderately low; 7) no association occurred for height of lower pod and maturity date, yield and flowering date, protein and maturity date, protein and height of lower pod, and yield and protein.

These correlations are somewhat lower than has been found in other studies with later generation material (9). The generally low or lack of associations of the characters flowering date, maturity date, and height of lower pod with yield or protein indicates that little or no progress could be made in improving the yield or protein by selecting for the above mentioned characters in the F_2 generation. Correlations of the characters that were highly significant did not account for enough of the variation to be of much use in selecting the associated traits.

Protein Behavior

The inheritance of protein content was quantitative in nature as was demonstrated by the wide range in protein content for the F_2 progeny. This has been well demonstrated in the frequency distribution tables by the fact that the protein content of the F_2 progeny could not be placed in a small number of qualitative classes. It was obvious that the easiest way to increase protein content of the progeny was through crosses between parents containing high protein content. Transgressive segregation occurred in most cross combinations. There was a strong tendency for the F_2 progeny to have a higher protein content mean than their respective midparent mean when two high protein lines were the parents. The protein content means of the F_2 progeny from two low protein parents tended to fall near the midparent mean. Although the protein content is important, other agronomic characteristics have to be considered when selecting for protein. However, no adverse correlations between protein and other characters were found in this study. Since yield is a very important character it also has to be considered when selecting for protein. It may be pointed out that selection for high yielding high protein lines may be accomplished by a plant breeder as has been pointed out by other researchers (20, 37).

There were several characteristics pertaining to protein which made it atypical of a quantitative trait. Eleven percent of the F_2 progeny exceeded the protein content range of the high protein parent, while 4% of the F_2 progeny fell below the range of the low protein parent. This indicates that transgressive segregation occurred since

15% of the F_2 progeny fell outside the protein content ranges of the parents. There was 1.5% of all the F_2 progeny above and 2% that fell below two standard deviations of their respective F_2 protein mean.

The mean protein content of the F_2 progeny of all crosses had a strong tendency to exceed the midparent means. Fifty-three percent of the F_2 progeny protein means were significantly higher than their respective midparent means while 4% of the F_2 progeny were significantly less than that value.

The data indicated that there were also other than additive effects which controlled protein content.

In order for a plant breeder to properly select for a particular character he should know the heritability of that character and how much progress he can expect to make by selecting a portion of one generation as parents for the next generation. The data showed that protein content had an overall high heritability (.70) and that progress can be made to increase protein content, even by selecting the higher protein progeny resulting from a cross between two high protein parents.

Correlation between Three Methods for Determining Protein in Soybeans

Three methods for determining protein in soybeans were compared in order to obtain an indication of the accuracy of the method used in this study for protein determination. The three methods that were compared were the Udy Dye Method, which was used for protein determinations in this study; Kjeldahl Total Nitrogen procedure; and the

Infrared Light Detection method. The correlation coefficients between these methods for protein determination are as follows:

Udy and Infrared = .96**
Udy and Kjeldahl = .93**
Infrared and Kjeldahl = .94**

All of the coefficients were positive, highly significant, and indicated a very strong association between the three methods for determining protein content. From this it could be concluded that the Udy dye method which was used in this study was an accurate method for determining protein content in soybeans (40, 75). Soybean seed are known to contain some nonproteinaceous nitrogen (40). Therefore, it is possible that the Udy method was as accurate or even more accurate than the Kjeldahl method because the Udy method is a measure of only the protein and not total nitrogen.

SUMMARY

A soybean (Glycine max (L.) Merrill), study was conducted with 10 parental lines differing widely in protein content, to determine F_1 hybrid performance and the heritability and relative combining ability of protein and other selected characters in the F_2 generation. Forty-five crosses were made between these parental lines, in all combinations, using the high protein parent where possible, as the female parent. The test was grown in 1973 on Olivier silt loam at Baton Rouge.

Significant differences were found among some of the parents grown with the F_1 and F_2 populations for protein content, maturity date, plant height and flowering date. Significant differences were also found among the F_1 and F_2 progeny, within their respective test, for all characters mentioned above. Significant differences for plant height and flowering date, were found among some F_2 progeny having the same female parent.

There was a tendency, in all but one case, for the F_1 progeny to vary in protein from the midparent mean, usually toward the high protein parent. Seventy-five percent of the F_1 progeny protein means exceeded their respective midparent mean in protein content. Thirty-six percent of the F_1 progeny exceeded their respective high protein parent. Heterosis for protein in 13 F_1 progeny averaged about one percent above the high parent. However, the F_1's of D67-6117 x Tracy and D68-4641 x Hutton had relatively good specific combining ability exceeding the high protein parent by 1.05 and .79%, respectively.

D67-6117 was the best parent for general combining ability with six of the eight F_1 crosses with it, exceeding the high protein parent. D68-4641 also had good general combining ability with five of the eight cross combinations exceeding the high parent. Twenty-five percent of the F_1 progeny protein means were less than their midparent. Nineteen percent of the F_1 progeny contained less protein than their respective low parent. Each of these F_1 progeny were derived from low protein x low protein parents with Pickett 71 and Bragg as one of the parents in three of the seven crosses. The F_1 progeny of Pickett 71 x Bragg was 1.04% lower in protein than the low parent.

This data indicates that other than additive gene action was involved in protein content of the F_1 progeny. Maternal and cytoplasmic effects may have caused the F_1 progeny to be skewed toward the high protein parent since the high protein parent was used as the female in most crosses.

Eighty-three percent of the F_1 progeny means exceeded their respective midparent maturity date mean and tended to be more like the later maturing parent. Fifty-three percent of the F_1 progeny had later maturity date means than their respective later maturing parent. Six percent of the F_1 progeny means were less than their respective midparent maturity date. Heterosis for maturity date as an average of the F_1 progeny exceeded the late parent by at least two days.

The F_1 progeny of all crosses except three, deviated from the midparent plant height means by at least 2 cm. Fifty-six percent of the F_1 progeny means exceeded their respective midparent in plant height by being more like the taller parent. Twenty-eight percent of the F_1 progeny were taller than their respective taller parent. Heterosis for

plant height for 10 F_1 progeny averaged 4.2 cm above the taller parent. The F_1 of Tracy x Pickett 71 and D67-6117 x Tracy had relatively good specific combining ability, exceeding the taller parent by 7.86 and 7.79 cm, respectively. Thirty-four percent of the progeny means were less than their respective midparent mean. Eleven percent of the F_1 progeny means were shorter than their respective shorter parent. This seems to indicate that other than additive gene action was involved in plant height of the F_1 progeny.

The flowering date and height of lower pod data for the F_1 progeny both had large coefficients of variation which were 24.32% and 30.37%, respectively.

There was a strong tendency for the F_2 progeny to have higher protein content means than their respective midparent mean. Fifty-three percent of the F_2 progeny protein means were significantly higher than their respective midparent mean while 4% were significantly less than that value. Eleven percent of the F_2 progeny exceeded the protein content range of the high protein parent while 4% of the F_2 progeny fell below the range of the low protein parent. This indicates that transgressive segregation occurred since 15% of the F_2 progeny fell outside the protein content ranges of the parents.

There was 1.5% of all F_2 progeny above and 2% below two standard deviations of their respective F_2 protein mean. The data indicated that there were also other than additive gene effects which controlled protein content.

Twenty-six percent of the maturity date means of the F_2 progeny tended to be like the later maturing parent by exceeding their midparent maturity mean by one or more days. Nine percent of the F_2 progeny

means were later in maturity than their respective later maturing parent. Forty-nine percent of the maturity date means tended to be like the earlier maturing parent by being earlier than the midparent maturity date mean by one or more days. Sixteen of the F_2 progeny means were earlier than their respective earlier maturing parent mean. Transgressive segregation occurred in several cases where 25% of the F_2 progeny had either later maturity means than their respective later maturing parent or earlier maturity date means than their respective earlier maturing parent. It also appears that gene action other than additive may have been partially responsible for these results.

Thirty-eight percent of the F_2 progeny had shorter plant height means than their respective midparent plant height mean by at least two cm. Twenty-two percent of the F_2 plant height means were shorter than their respective shorter parent plant height mean. Thirty-one percent of the F_2 progeny means tended to be taller than their respective midparent plant height mean by at least two cm. Sixteen percent of the F_2 plant height means were taller than their respective taller parent plant height mean. Transgressive segregation occurred since 38% of the F_2 progeny had either lower plant height means than their respective shorter parent or taller plant height mean than their respective taller parent plant height mean. The data indicated that there were also other than additive gene effects which controlled plant height.

Forty-seven percent of the F_2 progeny tended to have earlier flowering date means, by at least one day, than their respective midparent flowering date mean. Twenty-four percent of the F_2 progeny had earlier flowering date means than their respective earlier flowering parent. Eleven percent of the F_2 progeny had later flowering date

means, by at least one day, than their respective midparent flowering date mean. Four percent of the F_2 progeny had later flowering dates than their respective later flowering parent. Transgressive segregation occurred in several cases where 28% of the F_2 progeny had either earlier flowering date means than their respective earlier flowering parent or later flowering date means than their respective later flowering parent.

The height of lower pod data for the F_2 progeny had a large coefficient of variation of 39.73%.

Heritabilities as an average of all lines for protein, maturity date, plant height, flowering date and height of lower pod were .70, .50, .63, .76, and .46, respectively. Although there were some F_2 progeny that had low heritabilities for the selected characters, the data showed that good progress could be made for selection of these characters on an individual plant basis.

The expected advance was calculated for protein as a prediction of advance of a population mean by selection. The progeny of three crosses, all high protein x high protein crosses, had an F_3 predicted mean of over 52% protein.

The generally low or lack of association between the correlation coefficients of the characters flowering date, maturity date, plant height, and height of lower pod with yield or protein indicated that little or no progress could be made in improving the yield or protein by selecting for the above mentioned characters in the F_1 or F_2 generation. Correlations of the characters that were highly significant did not account for enough of the variation to be of much use in selecting the associated traits.

Three methods for determining protein in soybeans (Udy Dye; Kjeldahl Total Nitrogen; and Infrared Light Detection) were compared. Correlation coefficients of .96**, .94**, and .93** were all highly significant and indicated a very strong association between the three methods for determining protein content in soybeans.

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VITA

Theodore Calvin Miller was born September 29, 1938 in Eunice, Louisiana. He was graduated from Church Point High School in Church Point, Louisiana May, 1956. In June of 1956 he enrolled in McNeese State College at Lake Charles and received a Bachelor of Science degree in Agronomy in May, 1961.

He received a commission through the R.O.T.C. program and entered the Army in July 1961 as a Second Lieutenant in the Infantry. He remained on active duty in the Army for eight years during which time he served overseas in Germany, Korea, and Viet Nam. He attended and successfully completed the Army Aviators Fixed Wing School, the Army Rotary Wing School and a Method of Instruction course. Prior to medical retirement in December, 1970, he attained the rank of Major.

He entered the Graduate School at Louisiana State University in June of 1970 in the Department of Extension Education and received his Master of Science degree in August, 1971.

In September of 1971, he was accepted by the Department of Agronomy at Louisiana State University for further graduate study where he is now a candidate for a degree of Doctor of Philosophy.

He was married to the former Sally Jane Nordan on September 28, 1961 and now has a daughter, Deborah Lynn, age 13, and a son, Theodore Jr., age 10.

EXAMINATION AND THESIS REPORT

Candidate: Theodore Calvin Miller

Major Field: Agronomy

Title of Thesis: Combining ability of protein and other selected characters with the F_1 and F_2 plant generation of two-way crosses of ten soybean lines

Approved:

Curtis Wilcox
Major Professor and Chairman

James B. Traynham
Dean of the Graduate School

EXAMINING COMMITTEE:

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Date of Examination:

March 26, 1976